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/codon_start=1 /producl="hypothetical protein" /protein_id="cAB66591.1" /db xref="G1:13276639" /db xref="GOA:Q9BQIO" /db_xref="UniProt/TrEMBL:Q9BQIO" /translation="MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEEN	/note="hypothetical protein" 13381 /gene="hypothetical protein" 1541 /gene="DKFZp761J191" /gene="DKFZp761J191"	<pre>/mol_type="mRNA" /db_xref="RZPD:DKPZp761J191" /db_xref="taxon:9606" /clone="DKPZp761J191" /tissue_type="amygdala" /clone_lib="761 (Synonym: hamy2). Vector pSport1; DH10B; sites_NotI + SalI" /dev_atage_maxilt"</pre>	Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKF? further information about the clone and the sequencing available at http://mips.gsf.de/projects/cdna/. Location/Qualifiers 13381 ce /organism="Homo sapiens"	Direct Submission Direct Submission L Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp761J191) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.	Homo Homo Euka Mamm 1 Otte Mewe		47.6 3.2 780 5 BU945837 47.6 3.2 783 6 CA463011 47.6 3.2 784 6 CA463011 47.6 3.2 788 6 CA463011 47.6 3.2 788 6 CA463010 47.6 3.2 789 1 AU080330 47.6 3.2 800 1 AU080330 47.6 3.2 801 1 AU066891 47.6 3.2 802 1 AU066941 47.6 3.2 807 1 AU066941 47.6 3.2 807 6 CA46524 47.6 3.2 808 1 AU051621 47.6 3.2 808 1 AU051621 47.6 3.2 801 5 BU525307 47.6 3.2 824 5 BU938947 BU526307 BU526307 BU526307 BU526307 BU536307 BU536307 BU536307 BU536307 BU536307

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                                                                                                                                                                                                                                                         sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp761N011) is available at the KZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact KZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761N011 Further information about the clone and the sequencing project in the
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Mewes, H.W., Weil, B.,
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Location/Qualifiers
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                     /mol type="mRNA"
/db_xref="RZPD:DKFZp761N011"
/db_xref="taxon:9606"
/clone="DKFZp761N011"
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Osanger,A., Fobo,G.,
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LPEKLTAFKEKYMEFDLNNEGEILDMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDT
ISYRDFVNMMLGKRSAVLKLVMMFEGKANESSPKPVGPPPERDIASLP"
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89. .541
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DH10B; sites NotI + SalI"
/dev_stage="adult"
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/codon_start=1
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                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertomammalia; Eutheria; Primates; Catarrhini; Hot 1 (bases 1 to 1158)
Li,W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
  Genoscope.
Direct Submission
                           Faraday Avenue
2 (bases 1 to
                                                   Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                        CR601218 1158 bp mRNA line full-length cDNA clone CS0DJ009YG24 of T cells Cot 10-normalized of Homo sapiens (human). CR601218 CR601218.1 GI:50482025
                                                                                                                                                     Homo sapiens
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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CCATGGTTCCAGTGCTCTGGTGTCACCCAGGACACAGCCACTGGGGGCCCCGCTGCCCCA
                                           GAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTG
                                                          GAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTTCCTTGGACAGTG
                                                                                                   AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCT
                                                                                                                   AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCCAGGCCACTCT
                                                                                                                                                       GAGGCTTCCAGCCTGTGTTCCCCCTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAA
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/plasmid="pCMVSPORT_
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/tissue_type="T cells (Jurkat cell line)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                   Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EooR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced Contact: Genoscope
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2 rue Gaston Cremieux, CP 5706 -
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK004YL21"
/cell type="HBLA CELLS COT 2
/cell_line="HELA"
/clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                TGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCA
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93.1%;
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the DCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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1 (bases 1 to 958)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31263276.

Contact: Genoscope

Contact: Genoscope
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GCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCMCTGMGGGTTTGTTTTGTGTTTTCATCATGTCTTTGTAAAGCACAAATTATCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACATTGCTAGCCTGCCCTGAGGACCCCGCCTGGACTCCCCAGCCTTCCCCACCCCATAC
                                                                                                CTCCTTCCCCGCTCCCTGTGCAGAAGGGCTGACATCAAACCAAAAACTAGAGGGGGCAGG
                                                                                                                                   CTCCTTCCCCGCTCCCTGTGCAGAAGGGCTGATATCAAACCAAAAACTAGAGGGGGCAGG
                                                                                                                                                                                                                                                          CTTAAAGGGGCTCTGGGTCGGGGAA-TCCTGAGCCTTGGGTCCCCTCCCTCTCTTTCTTCC
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/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Flow prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958;
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FEATURES	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 6 BX400361 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	ρ ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο				, b & d & d
2 rue Gaston Cremitux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr. 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5100.f formation about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ009BD12QPl&c=5100.f. Location/Qualifiers	.5.	BX400361 BX400361 Homo Homo sapiens BX400361 BX400361	1375 GAATGAGAAATGCTCACGCAAAGTCAGGAGCACTGGTAAGCCAAGACTGAGAAA 1434 [CTGGGTANGGANGGTTGGGTTGGGTGTGGGTGTANGGANGG	599 GCCAGGGCAGGA-GCTTCCAGCCTGTGTTCCCCCTCACTTGGAGGAACCAGMACTCTCCA 541 896 TCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGACGACGACGACCC 955
1 2 1 2 1 6	•.	667 GGGTTTGTTGTTTCATCAACTGTGATCTCTTAAAGCACAAATTATCTGCCTTAAAGGGG	547 AGCCTGCCCTGAGGACCCCGCCTGGACTCCCCAGCCTTCCCAGCCCCATACCTCCCTC	OY 427 TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAA 486	OY 307 GACCTGATGTCTTTAAAGAGGATGATGAGAGAGCTTGGTGTCCCCAAGACCCACCTGGAG 366	ORIGIN Dispersed with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized." ORIGIN ORIGIN 55.8%; Score 828.4; DB 5; Length 894; Best Local Similarity 96.2%; Pred. No. 1.4e-207; Matches 855; Conservative 8; Mismatches 24; Indels 2; Gaps 2;	source 1894 /organism="Homo Bapiens" /db_xref="mRNA" /db_xref="cScDx00:9606" /clone="CScDx00:9424" /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /cell_tine="JURKAT" /clone_lib="Homo Sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) /rimer Fist strand cDNA was primed with a CDNA was

\$ \$ \$ \$ \$ \$ \$ \$ \$ \$	PEATURES SOURCE ORIGIN Query Mat Best Loca Matches	Db Db RESULT 7 BX374861 LOCUS DEFINITION ACCESSION VERSION KEYMODS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
20 CGGAGCCCGGACCAGGCGCCTGTGCCTCGTCCTCGTCCCTCGCCGCGAAGCCTG 79	8 1 0	781 CAGCTGATCCCCACTCATTYCACACCTCTTCTYATCCTCAGTGATGTGAAGGTAGGAAGG 840 11145 AAAGGAGCTTTGGGATGCCACTTCAAGAAGGTACCAGAAGGAACCC 1193
REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOUICE	Qy 6 Qy 7 Qy 7 Qy 8 Db 7	8 8 8 8 8 8 8 8 8 8 8 8
I (bases 1 to 1096) III-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collect Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informati found through the I.M.A.G.E. Consortium/LLNL at: http://image.llni.gov Plate: LLAM12711 row: h column: 07 High quality sequence stop: 666. 1. 1096 //organism="Homo sapiens" //mol_type="mRNA"	680 TTTTCATCATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGG 739 [TANAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAGAAGATGA 379

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ORIGIN
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Best Local Similarity
Matches 809; Conserv
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AAGGGCTGATATCAAACCAAAAACTAGAGGGGGCAGGGCC 838
                                                                                                 TTTCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTANAGGGGCTCTGGGTCGGGGA
                                                                                                                   TTTCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGA
                                                            ATCCTGAGCCTTGGGTCCCCTCTCCTCTTCCTTCCCTCCTTCCCCGCT-CCCTGTGCAG
                                                                                                                                                         accccdccriddacricccadccrrrcccaccccaraccrcccrcccdarcririccriderecrr
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size_2.1 kb, insert size range_1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code_036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:5723574"
/lab_host="DH10B"
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98.7%;
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Pred. No. 7.9e-196;
0; Mismatches 9;
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AUTHORS
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JOURNAL
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KEYWORDS
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segraté@genoscope.cns.fr
1st strand.cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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AL550606.3
EST.
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On Feb 15, 2001 this sequence version replaced gi:31272423. Contact: Genoscope
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                                                                                                                      TTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGGATCCGGACCAGGCGCCTGTGCCTCCTCGTCCTCGCCGCGTCCGCGAAG-CT 59
                                TTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAGAAGATG
                                                                                           TTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACCTGATGTCT
                                                                                                                                                                                      GAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAAGCTCACAGCC
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6.16
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ches 5;
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RESULT 10
CF454825
LOCUS
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
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                                                                      Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM583 row: j column: 10
High quality sequence start: 22
High quality sequence stop: 718.
Location/Qualifiers
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AGENCOURT 15463186 Lupski_anterior_horn Homo sapiens
IMAGE:30516609 5', mRNA sequence.
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1 (bases 1 to 832)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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/clone="IMAGE:30516609"
/tissue_type="Peripheral Nervous system"
/lab_host="DH10B (T1 phage-resistant)"
                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone lib="Lupski anterior horn"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed);
Site_2: NotI; Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 2.1 kb. Library was constructed by Invitrogen
and donated by J. Lupski, M.D./Ph.D. (Baylor College of
Medicine)."
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229 GAAGAGAACCTTCCAGAAAAAGCTCACAGCCTTCAAAGGAGAAGTACATGGAGTTTGACCTG
GGGTTTCCTTG 1019
                                                       TAGA-CCCAGGCCACTCTGAGAAGACCTTGGAGTAAGGACAATGCTGCAGGGGCTCTTTC
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                                                                               AGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTC
                                                                                                                                         CTCTCCATCCTTTCAGAAAGTCTCCAAGCCCAGTTCATGCTCACTGACCTGGCTCTGACG
                                                                                                                                                                 CTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACG
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842 bp

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REFERENCE
AUTHORS
TITLE
JOURNAL
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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High quality sequence stop: 721.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GGAGATGAAGAAGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCG
                                                                     GATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCT
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/lab host="pH108-Ton A ( T1 and T5 phage resistances)"
/lab host="pH108-Ton A ( T1 and T5 phage resistances)"
/clone lib="NIH MGC 181"
/clone lib="NIH MGC 181"
/clone to pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:30398267"
/tissue_type="White Matter"
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|mol_type="mRNA"
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Pred. No. 3.1e-18
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3.1e-187;
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                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
2 rue Gaston CDNA was disperted with Not I and cloned
2 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
2 was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Homin 1 (bases 1 to 755)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 13, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           955 bp mRNA
BX421987 Homo sapiens T CELLS (JURKAT CELL
clone CSODHO06YD09 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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BX421987.2
                                                                                                                                                                                                                                This sequence belongs to sequence cluster 5100.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODH006CB05QP1&c=5100.f.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i
                                                                                                                                                                                                                ocation/Qualifiers
                                                                             tissue type="T CELLS (JURKAT CELL LINE"
                                                                                                                                         mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                      clone="CSODH006YD09"
                                                                                                                                                                             organism="Homo sapiens"
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AGENCOURT 8965831 NIH_MGC_142
5', mRNA sequence.
BU597251
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                            Homo sapiens
                                                                     Homo sapiens (human)
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Pred. No. 2.9e-182;
5; Mismatches 0;
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2 Homo
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: NCI
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Pred. No. 1.3e-178;
0; Mismatches 12;
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                                                                                                                                                                                 Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Geneboosystems.com).
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 701)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to faci
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CA312962.1 GI:24531060
EST.
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                                                                                                                                                                                                                                                                                          University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
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                                                                                                                                                                                                                                                                                                                                                                                                                 discovery
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
uI-CF-FN0 is a subtracted cDNA library derived from two
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sapiens

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Homo sapiens

701 bp Lens cDNA

mRNA linear EST 01-AUG-2002 clone NT2RP4001514 5', mRNA

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TAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGACTGAGAAATACAAGGTTG
                                                                                         TAAAATGCTCACGGCAAAGTCAGCAGCACCAGGTAAGCCAAGAACTGAGAAATACAAGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6hr to LPS 24h
TAG_LIB=UI-CF-FN0
TAG_SEQ=CTGCTCAGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bento-soares@uiowa.edu
TAG_TISSUE=Human Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 normalized Human lung epithelial cell libraries (EN1 and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
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990 AGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGT	B 8
930 CACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACA	B 8
870 TCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCCAAGCCAAGTTCAGGCT	B &
810 TCANACCAAAAACTAGAGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCCC 	B 8
750 CTTGGGTCCCCTCCCTCTTCTTCCCTCCTTCCCCGCTCCTTGCAGAAGGGCTGATA	B 8
690 TGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCCTGAGC 	B 8
630 CTGTGATCTCTCTCTCTCTCATTTGTTTTGATGATTGAGGGTTTGTTGTTTTTCATCAACAA	8 8
570 GGACTCCCCAGCCTTCCCACCCCATACCTCCCGCGATCTTGCTGCCCTTCTTGACACA	B 8
xy Match 46.5%; Score 690; DB 1; Length 701; t Local Similarity 98.9%; Pred. No. 5.2e-171; ches 693; Conservative 0; Mismatches 8; Indels 0; Gaps	Quer Best Matc
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. ECATION/Qualifiers LOCATION/Qualifiers LOCATION/Qualifiers / Organisme"Homo sapiens" //db xref="mRNA" //db xref="mRNA" //clone="NT2RP4001514" //clone="NT2RP4001514" //cell_lipe="NT2RP4001514" //cell_lipe="NT2RP4" //clone_"NT2RP4" //clone_"Tokechor: pME185FL3; mRNA from NT2 neuronal precur cells after 2-weeks retinoic acid (RA) induction"	FEATURE 90
ĀL	JOURNAL COMMENT
Isogai T. HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nacai, T.	TITLE
ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. FERENCE 1 (bases 1 to 701) AUTHORS Ota, T., Sudiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J., AUTHORS Ota, T., Sudiyama, T., Nagai, T., Suzuki, Y., Saito, K., Yamamoto, J., AUTHORS Ota, T., Sudiyama, T., Nagai, T., Suzuki, Y., Saito, K., Yamamoto, J., AUTHORS Ota, T., Sudiyama, T., Nagai, T., Suzuki, Y., Saito, K., Yamamoto, J.,	ORGANIS

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661	1230	601	1170	541	1110	481
661 CTGAAANGCAGCGTGCAGCCCTACTGNCCCCTTACTGGGGCA 701	CTGAGAGGCAGCGTGCAGCCCTACTGTCCCCTTACTGGGGCA 1270	601 TCAAGAAGGTACCAGAAGGAACCCTTCAGTCCTGCTCTCTGGCCACACCTGTGCAAGCAG 660	1170 TCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAG	541 CTCTTCTCATCCTCAGTGATGTGAAAGGTGGGAAAGGAAAGGAGCCTTGGCATTGGGAGCCCT 600	1110 CTCTTCTCATCCTCAGTGATGTGAAGGTGGGAAGGAAGGA	481 CACCCAGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACAC 540

Search completed: March 29, 2005, 01:31:36 Job time: 5461 secs

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Patent No. 6135941

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Nue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
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US-09-049-672A-16
                                                                          US-09-049-672A-16
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3449 base pairs
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INPORMATION:
ARBERENCE/DOCKET NUMBER: PF-0497 US
REFERENCE/DOCKET NUMBER:
ATTORNEY/AGENT INPORMATION:
                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOTO4
CLONE: 1320068
                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-855-0555
                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-845-4166
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US-09-252-991A-7471
US-09-925-40-6405
US-09-902-540-6405
US-08-118-200-1
US-08-458-745-1
US-08-458-745-1
US-08-891-254-8
US-09-030-270A-8
US-09-030-270A-8
US-09-031-587-8
US-09-031-587-8
US-09-031-587-8
US-09-431-614-16
       Score 1445.6;
Pred. No. 0;
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07, Ap
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967 960 1027 1020	96 96 96	7 7 7 6	Dy 547 AGCCTGCCGGAGGACCCGGCTGGACTCCCAGCCCTACCCCATACCTCCCGG 606	427 420 487 480	ω ω 4· 4·		Matches 1459; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  Qy 7 ACACGCAGCTAGCCGGAGCCCGGACCAGGCGCTGTGCCTCGTCGTCGCCGCG 66
TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504 TELEPAX: 301-309-8439 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 632 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	FILING DATE: 21-JAN-1997  APPLICATION NUMBER: US 60/034,204  FILING DATE: 21-JAN-1997  ATTORNEY/AGENT INFORMATION:  NAME: JONACHAN L. Klein  REGISTRATION NUMBER: 41,119  REFERENCE/DOCKET NUMBER: PF353	MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPATING SYSTEM: PC-DOS/MS-DOS  SOFTMARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION NOMBER: US/09/010,147B  FILING DATE: 12-No. 6653445-2002  CLASSIFICATION DATA:  PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:	CORRESPONDENCES: 24  CORRESPONDENCE ADDRESS:  ADDRESSE: Human Genome Sciences, Inc.  STREET: 9410 Key West Avenue  CITY: Rockville  STATE: MD  COUNTRY: USA  COUNTRY: USA  COMPTIER READABLE FORM.	RESULT 2 US-09-010-147B-11 ; Sequence 11, Application US/09010147B ; Patent No. 6633445 ; GENERAL INFORMATION: ; APPLICANT: Ni et al. ; TITLE OF INVENTION: Human Proteins	Qy 1387 AAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCTAAGAATACAAGGTTGCT 1446	Qy 1267 GGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGTCAGCTC 1326	Qy 1087 GCTGATCCCCACTCATTCCACACCTCTTCTCATCCTCAGTGATGTGAAGGTGGGAAGGAA

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RESULT 3
US-08-361-441B-43
US-08-361-441B-43
; Sequence 43, Application US/08361441B
; Patent No. 6077948
; GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 88..5:

SEQUENCE DESCRIPTION:
US-09-010-147B-11
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STREET: 225 Franklin:
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                      NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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Pred. No. 5.4e-159;
0; Mismatches 2;
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US-08-792-013-5
| Sequence 5, Application US/08792013
| Patent No. 6204021
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SEQUENCE CHARACTERISTICS:
LENGTH: 491 base pairs
TYPE: nucleic acid
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Best Local Similarity 67.1%;
    GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Murry, Lynn E.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYTOKINES
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PRIOR DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
PILLING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/0
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/542-8906
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OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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Pred. No. 9.6e-44;
0; Mismatches 138;
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NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENCTH: 658 base pairs

TYPE: 100-1616-6616
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Best Local Similarity
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SOPTWARE: FRANCISEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,013
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION TOPORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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CORRESPONDENCE ADDRE
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STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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CLONE: 815614
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E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
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pred. No. 1.1e-43;
0; Mismatches 138;
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FEATURE:

; NAME/KEY: 525
; LOCATION: 525
; OTHER INFORMATION: n=a, 9
US-09-513-999C-3906
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEO ID NOS: 36681
SOFTWARE: PATENT. DM
SEQ ID NO 3906
LENGTH: 658
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FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
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NAME/KEY: CDS
LOCATION: 109..624
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ORGANISM: Homo sapiens
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Pred. No. 6.1e-42;
0; Mismatches 141;
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RESULT 6 US-09-513-999C-14979 ; Sequence 14979, Application US/09513999C ; Patent No. 6783961

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APPLICANT: Giordano, J.Y.

APPLICANT: Giordano, J.Y.

PATILE OF INVENTION: Expressed Sequence Tags and Enc.

PATENT NO. 6783961

PILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENT.pm

SEQ ID NO 14979
                                                                                                                                        RESULT 7
US-08-361-441B-4
Sequence 4, Application US/08361441B
Patent No. 6077948
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APPLICANT: Dumas Miline Edwards,
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
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                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n=a, 09-513-999C-14979
           APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 59
TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: 464
STREET:
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Boston
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Pred. No. 3.6e-41;
0; Mismatches 139;
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                                                                             CHRONIC ALLOGRAFT REJECTION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
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OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version
CURRENT APPLICATION DATA:
APPLICATION NDATA: US/08/361,441B
FILLING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILLING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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STRANDEDNESS: double
TOPOLOGY: linear
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                                  ATTGCTAGCCTGCCCTGA 558
                                                                                                                                            TCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCATCTTGAGAATGATTCTGATG
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                                                                      TATGAGGAGAAAAACAAAGA---ACACCAGAAGCCAACTGGTCCCCCAGCCAAGAAAGCT
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ATTTCTGAGTTGCCCTAA
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Pred. No. 2.2e-40;
0; Mismatches 151;
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RESULT 8 US-08-171-385-4

Sequence 4, Application Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. R

US/08171385

540

420 379 480 439

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APPLICANT:

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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ATTGCTAGCCTGCCCTGA 558
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                                                                                                                                                                                   CTGGAGATGAAGAAGATGATCTCAGAGGTGACAGTGACAGTGACACTATATCCTAC
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                                                                      TCTGACTTTCTCAGAATGATGCTGGGCAAGAGATCTGCCATCTTGAGAATGATTCTGATG
                                                                                                                                                            CTAGAGCTGAAGAAATTAATTAGAGAGGTGTCCAGTGGCTCCGAGGAGACGTTCAGTTAC
                                                                                                                                                                                                                      GATATCGATATTATGTCCTTGAAGCGAATGCTGGAGAAACTTGGGGTTCCCAAGACCCAT 319
                                                                                                                                                                                                                                                                                 CAGTCCAAACTGGAGGCCTTCAAGACGAAGTACATGGAGTTTGATCTGAATGGCAATGGA
                                          TATGAGGAGAAAACAAAGA ---ACACCAGAAGCCAACTGGTCCCCCAGCCAAGAAAGCT
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VENTION: Mediators of Chronic Allograft
VENTION: Rejection
SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.4;
Pred. No. 2.3
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APPLICANT: Dunds Wilne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANTION: Expressed Sequence Tags a
Patent No. 6783961
FILE REFERENCE: 59.USZ.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-09-513-999C-10617
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US-09-513-999C-10617
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US-08-171-385-1/c
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                                                  Sequence 1, Application US/08171385
Patent No. 5527884
Patent No. 5527884
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
Matches 205; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 507
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: 443
  STREET:
                    ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                      335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 СТGATGTСТТТАРАВСАГСАТСВАСВАВАСТТССТСТВОТССССВАСАСССТВОВАСАТС 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 CTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGAATTGAC 309
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                                                                                                                                                                                                                                                                                                             TIGCCCIGA
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Boston
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Pred. No. 1.2e-26;
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STATE: Massachusetts

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02110-2804

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RESULT 11
US-08-361-441B-1/c
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Best Local Similarity
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OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPETECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       APPLICANT: Russell, Mary E. APPLICANT: Utans, Ulrike TITLE OF INVENTION: MEDIATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraeer, Janie K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                            NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
COMPUTER READABLE FORM:
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                                                       STREET: 225 F:
CITY: Boston
STATE: MA
                  COUNTRY: USA
ZIP: 02110-2804
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TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                         GTCCCCAGCCAAGAAAGCTATTTCTGTATTGCCCTAA 52
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                                                                                                                                                                         MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.8; DB 1;
Pred. No. 1.7e-16;
0; Mismatches 97;
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                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-5139
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
SEQ ID NO 5139
LENGTH: 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5139, Approximately Patent No. 681233
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Best Local Similarity 63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/361
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,38
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/642-5070
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OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 TCTTGAGAATGATTCTGATGTGAGGAGAAAAACAAAGA---ACACCAGAAGCCAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 GCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGG-GTTCCCAAGACCCATCTAGAGCTGAAGAAATTAATTAGAGAGGTGTCCAGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSOCIATED
OF DETECTION AND USES THEREOF
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RESULT 14
US-09-949-016-16881
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US-09-949-016-5140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
                                                                                                                                     Sequence 16881, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION

FILE REFERENCE: CLOUISO7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5140
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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CURRENT FILING DATE: 2000-04-14
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o. 6812339
                                                                                                                                                                                                                                                          TTTCTCAGGATGATGCTGGGCAAGAGATCTGCCATCCTAAA 845
                                                                                                                                                                                                                                                                                                   TTTGTGAACATGATGCTGGGGGAAACGGTCGGCTGTCCTCAA 467
                                                                                                                                                                                                                                                                                                                                          CTAAAGAAATTAATTGGAGAGGTGTCCAGTGGCTCCGGGGAGACGTTCAGCTACCCTGAC
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Pred. No. 7.7e-12;
0; Mismatches 51;
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Pred. No. 7.7e-12;
0; Mismatches 51;
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                                                           DETECTION
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                                                           AND USES
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-16882
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; ORGANISM: Human
US-09-949-016-16881
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US-09-949-016-16882
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 00/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR RILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for
SEQ ID NO 16882
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                                                                                                                                                                                                                                                                                                                                                        GACCTGATGTCTTTAAAGAGGATGATGGAGGAGCTTGGTGTCCCCAAGACCCACCTGGAG 366
                                                                                                                                                                                                                            ATGAAGAAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGAC 426
                                                                                                                                                CTANAGANATTANTTGGAGAGGTGTCCAGTGGCTCCGGGGAGACGTTCAGCTACCCTGAC
                                                                                                                                                                                                                                                                                                        GATATCATGTCCCTGAAACGAATGCTGGAGAAACTTGGAGTCCCCAAGACTCACCTAGAG
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TTTCTCAGGATGATGCTGGGCAAGAGATCTGCCATCCTAAA
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                                                                    TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAA 467
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Novel human secreted
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Novel human secreted and
US2003092887-A1.
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Novel human secreted and
US2003088064-A1.
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US2003088071-A1.
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ADC47181 standard;
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US2003088066-A1.
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Novel human secreted and
US2003073816-A1.
17-APR-2003.
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                                                             Human cDNA encoding US2003099625-A1.
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Novel human secreted and transmembrane protein
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Human PRO polynucleotide
US2003096971-A1.
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Human cDNA encoding secreted/t
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ADD51265 standard; cDNA; Novel human secreted and US2003105289-A1.
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Human cDNA encoding secreted/transmembrane
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       Novel human secreted US2003045687-A1.
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                                                                                            ACA66895 standard; cDNA; 1485 BP.
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Human cDNA encoding secreted/transmembrane US2003082628-A1.
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Human cDNA encoding secreted/transmembrane
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US2003100717-A1.
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                                                                                             ADD75556 standard; cDNA;
Human PRO polynucleotide
US2003100064-A1.
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                        ADD74072 standard; cDNA;
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Novel human secreted and transmembrane
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(GETH ) GENENTERTH TWO
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                                           Human cDNA encoding US2003195347-A1.
                                                 ADE96568 standard; cDNA; 1485 BP.
Human cDNA encoding secreted/transmembrane
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ADH69669 standard; cDNA;
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                                                                            WO200274961-A1.
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Novel human secrete
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                                                                    26-SEP-2002
                                                                                                                                                                                                                   (GETH )
                                                                                                                                                                                                                                                                                               (GETH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nóvel human secreted
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) GENENTECH INC.
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98.5%;
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                    CDNA; 3381 BP.
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ID NO:17244.
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Human differentiation/development WO200198454-A2.

CDNA

clone amy2_1j19

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Query Match
Best Local (RSULT 131)
ID Ar 1
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Best Local Similarity
RESULT 124
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RESULT 130
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Best I
RESULT 1
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RESULT
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Tumour-associated antigenic target
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(GEHU-) GERMAN HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated protein US6135941-A.
                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 3825.
W0200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC66521 standard;
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                                                                                                                                                          Breast cancer prognosis WO2004065545-A2.
                                                                                                                                                                                                                                       Full length human cDNA useful EP1447413-A2.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI58050 standard;
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(INCY-) 1NCYTE PHARM INC.
97.3%;
ry Match
r Local Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                         Human breast specific WO200240672-A2.
                                                                                                                                                                                                                                                                                                                                            ABT03024 standard;
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                                                                                                                                                                                                      18-AUG-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
ry Match
92.6%; Sco
ry Match
94.9%; Pre
                                                                                                                                                                                                                                                                                                                  23-MAY-2002
      AAI96213 standard; cDNA; 768 BP.
Human neuroblastoma expressed polynucleotide
                                                                                  WO200166719-A1.
                                  (CHIB-) CHIBA PREFECTURE.

(HISM) HISAMITSU PHARM CO LTD.

43.4%; Sc
ry Match
Local Similarity 97.0%; Pi
                                                                                          duman neuroblastoma
                                                                                                     AAI96212 standard; cDNA; 781
                                                                                                                                        (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
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                                                                                                                      Local Similarity
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de SEQ
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marker #2540.
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for treating
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No. 0;
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No. 0;
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No. 0;
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No. 5.3e-169;
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Query Match
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RESULT 132
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RESULT 138
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RESULT 135
RESULT 139
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RESULT 137
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21Y Match 41.5%;
3t Local Similarity 92.0%;
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Human cDNA clone (5
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(HISM ) HISAMITSU PHAM CO LTD.

(A) 43.0%; SC

EXPY MATCH 43.0%; Property 1.5%; Prop
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                                                                                                                                                                                                                                                                                                                                                      ABX74821 standard; cDNA;
Human cDNA sequence #121
W0200279411-A2.
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cDNA encoding a ATG-1117 (allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intracellular calcium WO200210371-A1.
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                                                                                                                                                                                               Human breast specific WO200240672-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP879880-A1.
                                                                                                                                                                                                                                        ABT03023 standard;
                                                                                                                                                                                                                                                                                                                   (VAND-) VAN ANDEL INST.
                                                                                                                                                         (DIAD-) DIADEXUS INC.
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ch 30.4%;

l Similarity 99.8%;
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JONES L W.
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LABAT I.
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                                                              calcium ion transport
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(5'-primer)
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CDNA #1180.
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30.2%; Score
99.3%; Pred.
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96.4%;
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99.3%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 476.2; DB 9;
Pred. No. 4.1e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                          Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616;
No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      638.2; DB 4;
No. 2.8e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602.
                                                                                                                                                                                                                                                                                      348; DB
No. 2.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                448
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451.
No.
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                                                                                                                            278.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory
                                                                    related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4; DB
3e-115;
                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ν.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
..7e-161;
                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 2;
.3e-114;
                                                                                                                              ; DB 6;
                                                                                                                                                                                                                              IJ
                                                                                                                                                                                                                                                                                                                                                                                      CC-RCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                          10;
-86;
                                                                  DNA sequence SEQ
                                                                                                                                                                                                                                NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                      patients.
                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                          IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
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                                                                            NO:32.
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40200210371-A1.

куома накко косуо

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RESULT 147
ID ABK155
DE DNA en
PN US2002
PD 03-JAN
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RESULT 141
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             PADE
                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBBB
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                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                               W020022012.
12-DEC-2002.
(CLIN') CLINGENIX INC.
(CLIN') 12.9%; f
12.9%; f
                                                                                                              ABK15589 standard; cDNA;
DNA encoding novel human
US2002001827-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human allograft inflammatory WO9517506-Al.
                                                                                                                                                                                                        AAD05035 standard; cDNA; 659 BP.
NOVEL human cytokine-2 (NHC-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA65628 standard; cDNA; 491 Human allograft inflammatory US6077948-A.
                                         ADA67731 standard; Di
Novel human cytokine
                                                                                                       03-JAN-2002.
                                                                                                                                                                                     20-MAR-2001.
                                                                                                                                                                                               US6204021-B1.
                                                                                                                                                                                                                   AAD05035 standard; cDNA;
                                                                                                                                                                                                                                                                                           ADA19323 standard; cDNA;
Human insulin resistance
                                                                                                                                                                                                                                                                                                                                                                          AAV82802 standard; cDNA; 635 BP.
ATG-750/RC-9 (allograft inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP879882-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV82800 standard; cDNA; 635 BP.
ATG-750/RC-9 (allograft inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9722880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT64809 standard; cDNA; 635
Human RC-9 cDNA useful in pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD) HARVARD COLLEGE.
ry Match 12.9%;
rocal Similarity 67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD) HARVARD COLLEGE.
ry Match 12.9%;
r Local Similarity 67.1%;
                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
ry Match 12.9%;
Local Similarity 67.1%;
                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1997
                                                                                            (INCY-) INCYTE PHARM
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                       ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
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            INCYTE
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   GENOMICS
12.
                                                                                                                                                                                                                                                                                                                                                                                                        12.9%;
67.1%;
                                       DNA; 659 BP.
ne 2, NHC-2,
                                                                      INC.
12.9%;
67.1%;
                                                                                                                                                                                                                                                                                                                        12.9%;
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67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in proliferative
  .9%;
                                                                                                                        659 BP.
cytokine-2
                                                                                                                                                                                                                                                                                           639 BP.
marker IRM228
                                                                                                                                                                                                                                                                                                                                                                                                        d CORP.
k; Score
k; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
factor 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                       Score
Pred.
                                                                                                                                                       Score 192.2;
Pred. No. 7.9
                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                        Score 192.2; DB 2; Pred. No. 7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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Pred.
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Pred.
  Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                         DNA
                                                                       192.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192.
No.
                                                                                                                                                                                                                                       192.2; DB 1
No. 7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                         192.
No.
  192.2;
                                         #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192.
No.
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No.
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No. 6.4e-43;
                                                                                                                         (NHC-2),
                                                                                                                                                                                                                                                                                                                                                                           factor-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AIF-1) CDNA
                                                                       .2; DB 6;
7.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2; DB 2;
7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2; DB 2;
6.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                         .2; DB 2;
7.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2; DB 3;
6.8e-43;
                                                                                                                                                                                                                                                                                           (AIF1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arterial
                                                                                                                                                      ; DB 4;
.9e-43;
                                                                                                                                                                                                                                                 DB 10;
  BB
                                                                                                                         version
  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease
Length
                                                                                Length
                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA SEQ ID NO:43.
  659;
                                                                                                                                                                  659;
                                                                                                                                                                                                                                                                                                                                   635;
                                                                                                                                                                                                                                                                                                                                                                                                                   635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635;
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Best Local Similarity
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 154
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RESULT:153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 149
                                                                     RESULT 156
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Best Local
          Query Match
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                            ABK15587 standard; of DNA encoding novel lus2002001827-A1.
                                       Human secreted EP1033401-A2.
                                                                                                                                                                                                                          Human Mphi type 
JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                                   ADR52830 standard; DNA; 639 Drug therapy altered express WO2004072265-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR24778 standard; DNA; 639 BP. Breast cancer prognosis marker WO200406545-A2.
                                                            AAC03908 standard;
                                                                                                   (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                    AAH25798 standard; DNA; 4
Human Mphi type ibaI DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003031650-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene differentially regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK84357 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROT-) PROTEIN DESIGN LABS
xy Match 12.9%;
t Local Similarity 67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ22610 standard;
                                                                                                                                                                                  (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                (NECA-) NETHERLANDS CANCER IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA89946 standard; cDNA; 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004048938-A2.
                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
                                                                                                                                                                                                                                                                                                                      ) WYETH.
) BURCZYNSKI
                                                                                                                                                                                                                                                                                       DORNER A J.
Similarity
                    GENSET.
                                                                                                                                                                                                                                                                                                             TWINE N.
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                 protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sarcoma-upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%;
68.7%;
                                                                                                                                cDNA; 658 BP.
human cytokine-2
                                                                                                                                                                                                                                                                                        Σ
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                                                                                                                                                                                                                                                                                                                                                                                          CANCER INST.
12.9%; Scoi
68.7%; Prec
                                                                              INC.
12.6%;
65.2%;
                                                                                                                                                                                                                                                                                                                                                              NA; 639 BP. expressed
                                                                                                                                                               12.7%;
66.9%;
                                                                                                                                                                                                                                                                    12.9%;
68.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%;
68.7%;
 66
12
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3
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                                                 658 BP.
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expressed
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Pred.
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Pred.
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Pred.
Score
Pred.
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Pred.
                                                                                                                                                               Score 189.2; DB 4;
Pred. No. 4.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 191; DB 8;
Pred. No. 1.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        #639
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186;
No. 4
                                                                                                                                                                                                                                                                                                                                                                                            191;
No. 1.
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No. 1.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192.
No.
                                                                                                                                                                                                                                                                    191; DB 13;
No. 1.7e-42;
                                                  ü
                                                                                186.8; DB 6;
No. 2.5e-41;
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                                                                                                                                                                                                                                                                                                                                                               #181.
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                                                                                                                                  (NHC-2)
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                                                                                                                                                                                            SOCHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocytic
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DB 3;
.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
.7e-42;
                                                  3906
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                                                                                                                                  version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                              HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease
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                                                                                                                                                                                                                                                                                                                                                                                                      639;
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ВP

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Best Local Similarity
RESULT 165
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RESULT 159
                                                                                                                                                         RESUL
                                                                                                                                                                                                                                           RESULT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 158
                                                                                                                                                                                                                                                                                    Human insulin resistance marker W0200298355-A2.
                                                                                                                                                                                                                                                                                                                                                                              AAA65591 standard; cDNA; 627 BP.
Rat allograft inflammatory factor 1
US6077948-A.
                              AAH25805 standard;
Murine ibal(1-120)
                                                                                                                         AAH25804 standard; DNA; 441 Murine ibaI(EF1-EF1) DNA. JP2001078775-A.
                                                                                                                                                                                                                     Rat RC-9 cDNA useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003064624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB58279 standard; DNA; 653 Toxicity-related gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ99370 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH25799 standard;
Murine Mphi type il
JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC10904 standard; cDNA;
                    JP2001078775-A.
                                                                                                                                                                                                             WO9722880-A1.
                                                                                                                                                                                                                                 AAT64808 standard;
                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE.
ry Match 12.1%;
t Local Similarity 64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD) HARVARD COLLEGE.

ry Match 12.3%;
ry Match 65.1%;
                                                                                (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOKU-) KOKURITSU SEISHIN
(IYAK-) IYAKUHIN FUKUSAYO
                                                                                                                                                                                                                                                                        (CLIN-) CLINGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENE-) GENE LOGIC INC
                                                                                                                                                                                       SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOCHIDA PHARM CO LTD.
KOKURITSU SEISHIN SHINKEI CENT SOCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lard; cDNA; 627 BP.
inflammatory factor 1 (AIF-1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d; DNA; 44
ibaI DNA.
                                                                                                                                                                                                                      cDNA; 696
ul in proli
                                                                                                                                                                  BEECHAM CORP.
11.9%; Score
65.1%; Pred.
                                                            11.3%;
                                                                                                                                                                                                                                                    12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%;
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                                         360
                                                                                                                                                                                                                      ; 696 BP.
proliferative arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHINKEI CENT
HIGAI KYUSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 BP.
) ID 3305.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                         IRM228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182;
No. 5
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No.
                                                             167.8;
No. 4.2
                                                                                                                                                                   176;
No. ;
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No.
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No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                         182;
No. 5.
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:
                                                                                                                                                                                                                                                    7.4e-39;
                                                                                                                                                                                                                                                                                                                                       1.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2; DB
                                                            1.8; DB 4;
4.2e-36;
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2.4e-40;
                                                                                             SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KENKYU
                                                                                                                                                                                                                                                                                                         (AIF1)
                                                                                                                                                                    DB 2;
.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                         .5e-
                                                                                                                                                                             BB
                                                                                                                                                                                                                                                                                                                                                                                                                          10;
-40;
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                                                                                                                                                                                                                      diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                             NO:4.
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Query Match
Best Local S
RESULT 169
                                Best Loca
RESULT 173
                                                                                                                                 Best Loc
RESULT 172
                                                                                                                                                                                                                                                  Best Local Similarity RESULT 171
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RESULT 167
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RESULT 166
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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AAT64807 standa
Rat RC-9 gene v
WO9722880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH25800 standard;
Murine ibaI(1-115)
                                                                                           ADA67729 standard; Dr
Novel human cytokine
US2003096371-A1.
                                                                                                                                                                                                                                                                                                           AAV82799 standard; <
ATG-1100 (allograft
EP879882-A1.
                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein EP1033401-A2. 06-SEP-2000. (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH25803 standard; DNA; 4
Murine ibaI(EF2-EF2) DNA.
                                                                                                                                                                (KOKU-) KOKURITSU SEISHIN SHINKEI CENT
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                AAH25802 standard; |
Murine ibaI(30-120)
JP2001078775-A.
                                                                                                                                                                                                                                                             (SMIK) SMITHKLINE BEECHAM (
ry Match 8.8%;
t Local Similarity 66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2001078775-A.
27-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU
                                           (INCY-) INCYTE GENOMICS INC.
ry Match 8.5%;
t Local Similarity 65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC06542 standard; cDNA; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH25801 standard; DNA;
Murine ibaI(30-147) DNA.
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(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOCH ) MOCHIDA PHARM CO LTI
ry Match 11.0%;
t Local Similarity 68.1%;
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                                                                                                                                         Local Similarity
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IYAKUHIN FUKUSAYO HIGAI KYUSAI
MOCHIDA PHARM CO LTD,
MOCHIDA PHARM CO LTD,
5.6%; Score 143.
Similarity 64.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOCHIDA PHARM CO LTC
h 11.2%;
Similarity 67.6%;
           dard; DNA; ; useful in F
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ne 2,
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                                                                                                                                                                                                                                        DNA; 273
                                                                                                                                                                                                                             DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%;
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                                                                                                        639 BP.
NHC-2, I
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                        1678
            proliferative
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Pred.
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Pred.
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                                               Score
Pred.
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Pred.
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                                                                                                                                            127.8;
No. 4.8
                                               No. 1.8e-
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No.
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No. 2.7e-29;
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No. 7.1e-34;
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No. 7.1e-36;
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No. 6.4e-26;
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              arterial
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4.
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                                                                                                                                              4.8e-25;
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                                        ⊿ 9;
÷-24;
                                                          DB
                                                                                                                                                        DB 4;
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              disease
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              diagnosis.
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Al.

WYOWA HAKK.

A KYOWA HAKK.

A ST MATCH

AGEST LOCAL Similarity

RESULT 179

ID AAV82801 standa

DB ATG-1120 (a PN EP8738a PD 25-2
                                                                                    веят Local Similarity
RESULT 181
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                                                                                                                                                                                                                                                                                                                                     AAQ99371 standard; cDNA; 331 BP.
Rat allograft inflammatory factor 1
WO9517506-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 10806. W0200164835-A2.
                                                                                                                                                                                                                                AAV82801 standard; cDNA; 631 BP.
ATG-1120 (allograft inflammatory factor-1-delta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT64806 standard; DNA;
Rat RC-9 DNA useful in p
W09722880-A1.
AAA65588 standard; cDNA; 331
                                                                                                                                         WO200210371-A1.
                                                                                                                                                 ABL49900 standard; DNA; 117
Intracellular calcium ion tr
                                                                                                                                                                                                                                                                                                              Intracellular calcium ion transport related
                                                                                                                                                                                                                                                                                                                         ABL49899 standard; DNA; 117 BP.
                                                                                                                                                                                                                                                                                                                                                                                             Renal toxin progression gene marker #1419.
                                                                                                                                                                                                                                                                                                                                                                                                        ADP72830 standard; DNA; 424 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal kid
US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH42742 standard, cDNA;
                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
ry Match 7.7%; Sco
Local Similarity 59.7%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM (7.9%; ry Match 7.9%; Local Similarity 64.6%;
                                                                                                                                                                                                                                                                      7-FEB-2002.
KYOW ) KYOWA HAKKO KOGYO KK.
7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
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A/) LABAT I.
C/) STACHE-CRAIN I
                                                                                               KYOWA HAKKO KOGYO KK.
th 7.0%;
Similarity 93.2%;
                 HARVARD COLLEGE.
6.4%;
h
Similarity 63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney
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66.2%;
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62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 424 BP.
proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 BP.
#276.
                                                                                                                                                 transport
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; Score
; Pred.
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                                                                                                                                                            BP.
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Pred.
 BP.
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Pred.
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No.
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No.
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No.
                  94.8;
No. 8
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No. 3.7e-22;
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No.
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1.4e-23;
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3.7e-22;
                                                                                                 .2; DB 6;
1.2e-18;
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3.5e-22;
                   œ
                                                                                                                                                                                .2; DB 2;
4.5e-21;
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3.2e-22;
                  DB 2;
.5e-16;
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Best Local Similarity RESULT 190
                                                                                                        Query Match
Best Local Similarity
RESULT 189
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RESULT 183
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                                                                                                                                                    Breast cancer prognosis marker #1093.
WO2004065545-A2.
05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                           Human tumour-associated & WO2004060270-A2.
                                                                          ABK84756 standard; cDNA; 81800 BP. Human cDNA differentially expressed W0200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intracellular calcium ion WO200210371-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat allograft inflammatory US6077948-A.
       AAX89526 standard; o
                                                                                                                                                                                                                                                                  ADQ83815 standard; cDNA; 1363 BP. Human tumour-associated antigenic target WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP10331 standard; DNA; 1363 Reference mRNA sequences for
WO9934814-A1.
                                                                                                                                     (NOSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004042346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference mRNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP10462 standard; DNA; 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004042346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL49901 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-2000
                                                                                                                                                                                                                           (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW )
                                                                                                                                                                                                                                                                                                                                                                                                                             (EXPR-) EXPRESSION DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
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5h
6.4%;
Similarity 63.7%;
                                                        GENE LOGIC
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No. 3
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No. 3
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No. 2
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                                                                                    granulocytic
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.4e-11;
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.4e-11;
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.4e-11;
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.4e-11;
                                       DB 6;
.6e-10;
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.4e-14;
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.5e-16;
                                                                                                                                                                                                                                                                              (TAT)
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Best Local Similarity RESULT 198
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Best Local Similarity
RESULT 191
                    RESULT 199
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RESULT 194
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RESULT 193
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                                                                                      Human cDNA upregulated US2003134283-A1.
                                                                                                                                  19-SEP-2001.
(SHAN-) SHANGHAI INST ONCOLOGY.
4.6%; Score
                                                                                                                                                                 CN1313316-A.
                                                                                                                                                                           ABA04457 standard; cDNA; 1923
Human PP3051 protein encoding
                                                                                                                                                                                                                                             Tumour-associated antigenic WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                              Novel human arginine-rich US2004053250-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide WO200270539-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH18153 standard; cDNA; 1876 BP.
Human cDNA sequence SEQ ID NO:18038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001
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EP1074617-A2.
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                                                                                                         ADB47517 standard; cDNA; 1924 BP
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                                                                                                                                                                                                                                                                  ACN37848 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH08134 standard;
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ABA04454 standard; cDNA; 1562 BP.
Auman PP1187 protein encoding cDNA SEQ ID NO:10/12.
                                                                   PETE/) PETERSON D
                                                                              .7-JUL-2003
                                                                                                                                                                                                                                                                                                       DRMA/) DRMANAC R T.
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                                                                                                                                                                                                                                                                                                                                                                 1DM44080 standard; cDNA; 1897
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SEQ ID NO:4969.
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cDNA SEQ ID NO:19/21
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No. 1.
                            68.8;
No. 3.
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No. 3.
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.7e-08;
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.7e-08;
                            DB 10;
.7e-08;
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.7e-08;
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.7e-08;
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.5e-10;
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.6e-08;
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Best Local Similarity
RESULT 200
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RESULT 205
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RESULT 204
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RESULT 201
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RESULT 206
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                                                                                                                                                                                              Human prostate cancer cDNA #401. US2003190640-A1.
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19-SEP-2001.
(SHAN-) SHANGHAI INST ONCOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                     ADK51980 standard; cDNA; 2277
Human atopic dermatitis/psoria
WO2004016785-A1.
                                                                                                                                                                                                                                                                                 Tumour-associated WO2004030615-A2. 15-APR-2004.
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(AUCK-) AUCKLAND UNISERVICES
27 Match 4.3%;
It Local Similarity 59.7%;
                                                   ADI30758 standard;
                                                                                                                                   ACC79092 standard;
                                                                                                                                                                                                                                                                                                    ACN37282 standard; cDNA; 2277 BP.
Tumour-associated antigenic target
                                                                                                                                                                                                                                                                                                                                                        (UYJU-) UNIV JUNTENDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004018969-A1.
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ry Match 4.3%;
t Local Similarity 59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK43437 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV41920 standard; cDNA; 582 BP Nucleotide sequence of the cDNA
                             US6607879-B1.
                                                                                            (INCY-)
                                                                                                     27-FEB-2003
                                                                                                                WO2003016506-A2.
                                                                                                                      ACC79092 standard; cDNA;
Human secreted protein SE
                                                                                                                                                                            (FARI/) FARIS M.
(PEAR/) PEARSON C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004.
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                                                                                                                                                                                                                                                   ocal Similarity
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 Match
          INCYTE
                                                                                           INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                       GENENTECH INC.
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          CORP.
                                                                                                                                                                                                                                                  4.3%;
59.7%;
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59.7%;
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                                                  CDNA; 1358
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59.7%;
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59.7%;
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59.7%;
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4.3%;
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SECP-67
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Pred.
Score 63.2;
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Pred. No. 7.9e-07;
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No. 3.
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.1e-07;
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.6e-07;
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.7e-07;
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.9e-07;
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RESULT 216
ID ABL498
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PN WO2002
PD 07-FEE
PA (KYOW
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                                                                                                                                                                                                                                                                                                               Human PRO polynucleotide US2004014039-A1.
                  Intracellular calcium WO200210371-A1.
                                     ABL49898 standard;
                                                                                            Intracellular calcium ion transport WO200210371-A1.
                                                                                                             ABL49897 standard;
                                                                                                                                                                             ABL30333 standard; DNA; 1000 BP.
Drosophila melanogaster genomic polynucleotide
                                                                                                                                                                                                                                                WO200210371-A1.
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ry Match 4.2%;
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Drosophila melanogaster genomic polynucleotide
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                          Human brain expressed single WO200157275-A2.
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(MOLE-) MOLECULAR DYNAMICS INC.
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(MOLE-) MOLECULAR DYNAMICS INC.
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Human liver single
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Probe #2629 used to
WO200157272-A2.
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Human foetal liver
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Best
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Best Local Similarity
RESULT 243
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RESULT 240
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RESULT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAI02500 standard;
Probe #2491 used to
WO200157270-A2.
                                     Plant DNA sequence WO2003020936-A1.
                                                                                                    DNA homologous to phytopathogen WO2003020905-A2.
                                                                                                                                                                 DNA homologous to WC2003020905-A2.
                                                                                                                                                                                                                               DNA homologous t
WO2003020905-A2.
                                                                                                                                                                                                                                                                                             Human immune system WO200200928-A2.
                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS:
ry Match 3.7%;
t Local Similarity 72.9%;
                                                                                                                                                                                                                                                                                                                                                                 ABS02484 standard; DNA; 500 Human genome-derived single
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WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABS27607 standard;
                                                     ADK57002 standard;
                                                                                                                     ADC76478 standard;
                                                                                                                                                                                                                                              ADC75907 standard;
                                                                                                                                                                                                                                                                                                            ABL32566 standard; DNA; 6907
                                                                                                                                                                                                                                                                                                                                                          WO200186003-A2.
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                                                                                    (DOWC ) DOW CHEM CO.
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th 3.7%;
Similarity 72.9%;
Similarity
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phytopathogen
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phytopathogen
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o measure
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which
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No. 0.
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51.8;
No. 0.
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.0012;
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.0012;
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.0002;
DB 1
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Query Match
Best Local S
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RESULT
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PD 03
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Best Local :
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13-MAR-2003.
(DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
(DOWC ) DOW AGROSCIENCES LC.
3.3%; S
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Plant DNA
                                                                                          ADB52516 standard; DNA; 691 BP. Primary rat hepatocyte toxicity
               Rice gene,
                                                                                                                                                                                                                                                                               (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
ry Match
3.3%;
ry Match
50.0%;
                           ADA71938 standard; DNA; 2000
                                                                                  WO2003065993-A2.
                                                                                                                   )7-AUG-2003.
(GENE-) GENE LOGIC INC.
3.3%;
ry Match 3.3%;
50.4%;
                                                                                                                                                            Toxicity-related gene, WO2003064624-A2.
                                                                                                                                                                             ADB58040 standard; DNA;
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                                                                                                                                                                                                                                                                  ADK55190 standard; DNA;
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Plant DNA sequence which WO2003020936-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK59086 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA homologous to phytopathogen resistance-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC77196 standard; DNA; 620 BP.
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th 3.3%;
Similarity 50.0%;
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                                                    J INC.
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phytopathogen
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No. 0.0048;
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Query Match
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RESULT 257
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RESULT 255
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AAC03907 standard; cDNA; :
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Maize sucrose synthase US2003135870-A1.
                                                                              Rice gene,
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                                                                                                                                                                                                                                                                                                        ADL07540 standard;
                                                                                                                                                                                                                                                                                                                                                             Human secreted protein 5' EP1033401-A2.
                                                             03-JAN-2003
                                                                    WO2003000898-A1.
                                                                             ADA71938 standard;
Rice gene, SEQ ID S
                                                                                                                                           WO2004048938-A2.
                                                                                                                                                   Human soft tissue
                                                                                                                                                             ADQ23762 standard;
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                NDA58445 standard;
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PROVART N.
RICKE D.
ZHU T.
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GOFF S A.
KATAGIRI F.
                                 SYNGENTA PARTICIPATIONS AG.
h 3.1%; Score 45
Similarity 9.9%; Pred. No.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                         PROTEIN DESIGN LABS
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                                                                                                                                                                                                                                                                                               Troponin
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3.1%;
y 51.5%;
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51.5%;
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3.1%;
46.8%;
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51.5%;
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EST, SEQ
        03 BP.
#89.
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Pred. No. 0.
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No.
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0.011;
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0.054;
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Best
RESULT
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                                                                          RESULT
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RESULT 266
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         Query Match
Best Local :
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                                                                                                                                                                            AAH98302 standard; c
Human EST-derived cc
WO200154477-A2.
02-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                               Human hyperpolarisation-activated W020020330-A2.
                                            Maize gene conferring WO2003000906-A2.
                                                                                                                                                                                                                                                                                  Human tumour-associated WO2004060270-A2. 22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                      Human HCN2 cDNA. WO200159153-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Renal toxin progression WO2004048598-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200295000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABT41999 standard;
Toxicity modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003.
(GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toxicity-related gene, WO2003064624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB58316 standard; DNA; 1112 I
Toxicity-related gene, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2003
                                                                                                                                                                                                                                                                                                               ADQ83419 standard;
                                                                                                                                                                                                                                                                                                                                                                                         AAH48729 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP72640 standard; DNA; 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                ADA49154 standard;
                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENE LOGIC INC.
TY Match
Local Similarity 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE LOGIC
                           (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                    SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                    AVET ) AVENTIS PHARMA DEUT
Local Similarity 269
                                                                                                                                                            Local Similarity
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                                                                          Æ BEECHAM PLC.
3.0%; Score 4/
                                                                                                                                                                                                        ; cDNA; coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INC.
3.0%;
49.8%;
                                                                                                                                                                                                                                                                                                                                                                                          CDNA; 3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 1112 BP. related rat g
                                                                                                                                                           3.0%;
57.6%;
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49.8%;
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57.6%;
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         3.0%;
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57.6%;
                                                        disease
                                                                                                                                                                                                                                                                                                     ; 3372 BP.
antigenic
                                                                447 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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sequence
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D 3342.
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                                                                                                                                 cyclic nucleotide-gated channel 2
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No. 0.
         44.4;
No. 0.
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No. 0
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No. 0
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No. 0.
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No. 0.
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No.
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0.12;
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0.12;
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0.12;
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.28;
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.28;
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.12;
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Best Local Similarity
RESULT 271
ID ADMAN
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Best Loca
RESULT 272
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                                                                                              RESULT
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA49026 standard; DNA; 787 BF Wheat gene conferring disease
                                                         Plant cDNA #3639.
US2004016025-A1.
22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant
                                                                                       ADJ42639 standard;
                                                                                                                                                                                                                                               US2004016025-A1.
                                                                                                                                                                                                                                                                   ADJ42636 standard;
                                                                                                                                                                                                                                                                                                                                                                                              (MOUG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ42631 standard; cDNA; 787
Plant cDNA #3631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003135888-A1.
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Wheat cDNA modulated by post-transcriptional
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                             BRIG/)
                                       Moug/)
                    COOP/)
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                            MOUGHAMER T.
BRIGGS P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                         BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
KREPS J.
FROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNGENTA PARTICIPATIONS AG. h 3.0%; Score 44.4; Similarity 50.5%; Pred. No. 0
BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
                                                                                                                                                                                                                                                                                                        RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANG H.
BRIGGS S I
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KATAGIRI F.
KREPS J.
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                                                                                                                                                                                                                                                                                     Similarity
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GOFF S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUGHAMER T. PROVART N.
                                                                                                                                                                                                                             SUDWORTH P.
                                                                                                                                                                                                                                                         #3636.
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50.5%;
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No. 0.
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RESULT 282
ID AAS44950 standard; cDNA; 2247 BP.
DE cDNA encoding novel human secretory protein, Seq ID No
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                             BBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 274
                                                                                                        RESULT 281
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                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian specific g WO2004013311-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN83907 standard;
Calcium sensor G85
EP1209167-A1.
                                                                                                                                                                 ABD21000 standard; DNA; 2190 Human calmodulin 2 DNA.
                                                                                    ADN60285 standard;
Human calmodulin 2
                                                                                                                                                                                                                                WO200285308-A2.
31-OCT-2002.
                                                                                                                                                                                                                                                Human calmodulin 2 gene.
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                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC.

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ry Match

49.2%;
                                                                                                                                                                                                                                                                                                                                 Human cDNA differentially expressed in
                                                                                                                                                                                                                                                                                                                                           ABK83767 standard; cDNA; 2175 BP.
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                                                                                                                (EPIG-) EPIGENESIS PHARM INC.
ry Match 3.0%;
t Local Similarity 49.2%;
                                                                                                                                                                                               (EPIG-) EPIGENESIS PHARM INC.
ry Match 3.0%;
Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                       WO200228999-A2.
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(OKAZ-) OKAZAKI NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZHUT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIAD-) DIADEXUS INC.
                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
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PROVART N.
RICKE D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KATAGIRI F. KREPS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 1251 encoding s
                                                                                  cDNA; 2190 BP.
encoding cDNA.
                                 4 INC.
3.0%;
49.2%;
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3.0%;
49.2%;
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58.3%;
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0.33;
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0.27;
                                   DB 13;
0.33;
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0.33;
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0.33;
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0.16;
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0.27;
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      31
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Query Match
Best Local S
RESULT 283
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Best Local Similarity
RESULT 288
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RESULT 286
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Best Local Similarity
RESULT 285
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Best Local Similarity
RESULT 284
                                                                                                                                                                                                                                                                                                                                               ABL63305 standard; DNA; 1161 Breast cancer related gene so WOZ00194629-A2.
                                                                                                                                                            AAX90998 standard; DNA; 6710 Human centrin-2 genomic seque W09951186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ84750 standard; cDNA; 2363 BP. Human tumour-associated antigenic W02004060270-A2.
AAC55847 standard; DNA; Mitomycin biosynthetic sw0200053737-A2.
                                                                                        ADT66612 standard; cDNA; 1084 Rat calmodulin cDNA.
                                                                                                                                                                                                                                                                 Human centrin-2 gene WO9951186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ86930 standard; cDNA; 2363 BP. Human tumour-associated antigenic WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200166689-A2
                                                                             WO2004070383-A2.
                                                                                                                                        (MILL-) MILLENNIUM PHARM INC (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                          (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize sucrose
                                                           (CHEF ) GRUENENTHAL
                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                           AAX90997 standard; DNA; 1173 B
Human centrin-2 gene (Hcen-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA58674 standard; cDNA; 255 BP. Waize sucrose synthase EST #318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH (WUTD/) WU T D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                             (AVAL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                        Local Similarity
                                      ocal Similarity
                                                                                                                     ocal Similarity
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                                                                                                                                                                                                                                                                                                                             AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
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                                                                                                                                                                                                                                                                                                        2.9%;
52.8%;
                                     . GMBH.
2.9%;
49.3%;
                                                                                                                                                                                                              2.9%;
                                                                                                                   2.9%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                       2.9%;
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49.2%;
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49.2%;
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9
       gene
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         cluster
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Pred.
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Pred.
                  ВÞ
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Pred.
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                                                                                                                                                                                                              43.6; DB
No. 0.31;
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No. 0.
                                      43.
No.
                                                                                                                     No.
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No.
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         related
                                                                                                                                                                                                                                                                                                       3.6;
                                      . . 4
                                                                                                                     .6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                          IJ
                                                                                                                                                                                                                                                                                                       DB
.31;
                                      DB
34;
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.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                           NO:1642
        alpha
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                                                                                                                                                                                                                       Length
         amylase orf20
                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence #3805.
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Desc Local Similarity
RESULT 291
Query Match
Best Local Similarity
RESULT 297
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RESULT 293
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PA
PA
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RESULT 294
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                                                                                                                                                     Best Local Similarity
                                                                                                                                                                         Query Match
                                                                                              Query Match
                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                       (FISH/) FISHER D K. (LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000.
(MINU ) UNIV
                            03-JUN-2004
(CNSJ ) CON
                                                       ADO21558 standard; DNA; 450 BP. Calmodulin mutant Y99F/Y138F-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC55841 standard;
Complete Mitomycin
WO200053737-A2.
                                                                                                                          EP1209167-A1.
                                                                                                                                  ABN83905 standard; cDNA; 447 BP. Rat calmodulin encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. lavendulae gene
US2003134398-A1.
                                              WO2004046179-A1.
                                                                                                                                                                                                                                                                                                                               US2003134398-A1.
17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE10328 standard;
                                                                                                                                                                                                                        US2003135870-A1.
                                                                                                                                                                                                                                 Maize sucrose synthase
                                                                                                                                                                                                                                                                                                                                                           ADE10260 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HEMM/) HE M.
(SHEL/) SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (/YOAM)
                                                                                                                                                                                                                                          ADA58464 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHER/) SHERMAN D H.
(MAOY/) MAO Y.
(VARO/) VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                SHEL/) SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMM/) HE M.
                                                                                                      OKAZ-) OKAZAKI NAT
                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                  lavendulae mitomycin
                                                                                                                                                                                                                                                            ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV MINNESOTA.
SHERMAN D H.
                                                                                                                                                                                                                                                                                                                    SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                            SHERMAN D H.
MAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAROGLU M.
HE M.
                                                                                                                                                                                                                                                                                           HE M.
                                                                                                                                                                                                                                                                                                            MAO Y
                                                                                                                                                                                                                                                                                SHELDON P.
           CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

n 2.9%; Score 43.2; DB 12;
Similarity 50.5%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                   VAROGLU M.
                                                                                                                                                                                                                                            cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 18034
ORF 11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 2466
for orf20
                                                                                   RES INST.
2.9%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.9%;
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EST "
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C gene cluster
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#108.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                     Score
Pred.
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No. 1
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No. 0.
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No. 0.
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No. 1
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No. 0.
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.2;
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.51;
                                                                                     .25;
                                                         SEQ
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                                                          NO:5.
                    Length
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                                                                                               447;
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                                                                                                                                                                                                                                                                                                                                                                                         18034;
                     450;
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Query Match
Best Local S
RESULT 305
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Best Local S
RESULT 300
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RESULT 303
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RESULT 299
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RESULT 298
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RESULT 302
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RESULT 304
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT 2.9%; Local Similarity 54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD45852 standard; cDNA; 2908 BP.
Corn sucrose synthase (Sus1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF60791 standard;
BCC DNA #SEQ ID 13.
WO2003076466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EP1033401-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO21556 standard; DNA; 450 BP. Calmodulin mutant Y138F-encoding DNA,
                  AAA31901 standard; DNA; 495 Plant microsatellite marker W09967421-A1.
                                                                                                                                                                                                                     Plant microsatellite WO9967421-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC03838 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CNSJ)
                                                             (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FOREST I

TY Match
Local Similarity 48.9%; Pred.
                                                                                                                     WO9967421-A1.
                                                                                                                                AAA31434 standard; DNA; 450 BP.
Plant microsatellite marker #395.
                                                                                                                                                                                                            29-DEC-1999
                                                                                                                                                                                                                                            AAA31581 standard;
                                                                                                                                                                                                                                                                                     (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                 Maize sucrose sy
US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200267662-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEUR-) NEUROGENEX CO LTD.
ry Match 2.9%;
t Local Similarity 50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CNSJ)
                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD (FLET-) FLETCHER CHALLENGE FOREST 1
                                                                                                                                                                                                                                                                                                                                                       ADA58522 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONSEJO SUPERIOR INVESTIGACIONES h 2.9%; Score 43.2; Similarity 50.5%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONSEJO SUPERIOR INVESTIGACIONES h 2.9%; Score 43.2; Similarity 50.5%; Pred. No. 0
 GENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID 13.
                                                                                                                                                                                                                                                                                                                                            synthase
 RES
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Y99F-encoding DNA,
                                                                                                                                                                                                                                  DNA; 378
te marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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54.8%;
 VEC
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EST #166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182
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 CORP
                                BP.
#862.
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#542.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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No. 0
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                                                                   No.
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No.
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                                                                                                                                                                                                                                                                   DB 9;
0.23;
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                                                                                                                                                                  DB 3;
0.26;
                                                                  0.28;
                                                                            BB
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DB 12;
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RESULT 310

ID ADC75909 standard; DNA; 624 BP.
DE DNA homologous to phytopathogen
BN W02003020905-A2.
PD 13-MAR-2003.
                                                                                    PA PR DE PA
                                                  Query Match
Best Local Similarity
RESULT 312
                                                                                                                                                                                                                                     BREE
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PA
PA
PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 307
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                             ADC77180 standard;
DNA homologous to p
WO2003020905-A2.
                                ADK56990 standard;
Plant DNA sequence
                                                                                                             Plant DNA sequence which
                                                                                                             ADK59089 standard; DNA; 624 BP.
Plant DNA sequence which confers altered
                                                                                                                                                                         DNA homologous to phytopathogen resistance-related WO2003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADA58468 standard; cDNA;
Maize sucrose synthase E:
US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ42635 standard;
Plant cDNA #3635.
                         WO2003020936-A1.
                                                                                                       WO2003020936-A1.
                                                                                                                                                                                                                                                                                                                                    US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                            Maize sucrose synthase EST #99.
                                                                                                                                                                                                                                                                                                                                                                                      (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FLET-) FLETCHER
                                                                                                                                                         (DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004016025-A1.
                                                                                                                                                                                                                                                                                                         CHEI/) CHEIKH N.
FISH/) FISHER D K.
                                                                                                                                                                                                                                                                                                                                                     DA58455 standard;
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                                                                                                                                        ocal Similarity
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                                                         DOW AGROSCIENCES LLC.
th 2.9%;
Similarity 50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                             DOW CHEM CO
                                                                                                                                                                                                                                                                                                  LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLAZEBROOK J.
        CHEM CO
                                                                                    CHEM CO
AGROSCIENCES LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHALLENGE FOREST LTD.
                                                                                                                                                                                                                                                     ; DNA; 624 BP.
phytopathogen
                                                                                                                                                                                                                                                               DNA;
                                DNA; 624 BP. which confers
                                                                                                                                                                                                                                                                                                                                                     CDNA; 313 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 820
                                                                                                                                       2.9%;
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50.7%;
                                                                                                                                                                                                                                                                                2.9%;
54.9%;
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EST #112.
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Pred. No.
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Pred.
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Pred.
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Pred.
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                                 altered
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No. 0.
                                                           No.
                                                                                                                                        42.6;
No. 0.
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No. 0.
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No. 0.
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0.3;
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.43;
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.43;
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.44;
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. 43;
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31;
                                 metabolic
                                                                                                              metabolic
                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 820;
                                                                  Length
                                                                                                                                              Length
                                                                                                                                                                                                                   Length
                                 characteristic #4373.
                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                      CDNA
                                                                                                              characteristic #6472.
                                                                                                                                                                                                                    624;
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Query Match
Best Local S
RESULT 321
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RESULT 315
                                                                                                            Best Local Similarity RESULT 320
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RESULT 319
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RESULT 317
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RESULT 314
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                                                                                                                                  Query Match
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13-MAR-2003.

(DOWC ) DOW CHEM CO.

(DOWC ) DOW AGROSCIENCES LLC.

2.8%; S.

Match ....itv 48.2%; F.
                                                                                                                                                                                                                             (DOWC )
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC77187 standard;
DNA homologous to I
WO2003020905-A2.
                                                                                                                                                                                                                                                ADK59090 standard; DNA; 6
Plant DNA sequence which
WO2003020936-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                    ADK56997 standard; DNA; 6 Plant DNA sequence which WO2003020936-A1.
Nucleotide sequence WO200146387-A1.
        AAH74541 standard; cDNA;
Nucleotide sequence of a
                                                                                        ADT66614 standard;
Murine calmodulin
                                                                                                                     (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON ry Match 2.8%; Score 41.8; I Local Similarity 48.9%; Pred. No. 1.1
                                                                                                                                                              Mouse ischaemic condition WO200188188-A2.
                                                                                                                                                                          ABI99274 standard; cDNA; 1361 BP. Mouse ischaemic condition related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA homologous t
WO2003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003020936-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse cancer ass WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ97470 standard;
                                                            (CHEF ) GRUENENTHAL
                                                                                WO2004070383-A2.
                                                                                                                                                        22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2003
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DOWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC75903 standard; DNA; 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK55193 standard;
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ry Match 2.8%;
t Local Similarity 47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L3-MAR-2003
                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 674
sequence which con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ndard; DNA; 28516 BP.
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                                                                                         cDNA; 1361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phytopathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                              phytopathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                     , GMBH.
2.8%;
48.9%;
                                                                                                                                                                                                       2.8%;
48.2%;
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48.2%;
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50.7%;
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                                                                                                                                                                                                                                                                                                                                                                          695
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                                                                                                                                                                                                                                                                  695 BP.
n confers altered metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 8*;
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        905 BP.
chitobiosidase
                                                                                                                                                                                                                                                                                                                                                               confers altered metabolic
                                                                                                                                                                                                                                                                                                                                                                          BP.
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Pred.
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Pred.
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Pred.
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                                                                                                                       41.8; DE No. 1.1;
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No. 0.
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No. 0.
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No. 0.
                                      41.8;
No. 1.
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No. 0.
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No. 0.
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No. 0.
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                                                                                                                                                                        sequence
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        polypeptide
                                   DB . 1,
                                                                                                                                                                                                      DB
.76;
                                                                                                                                                                                                                                                                                                DB
.76;
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.76;
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.75;
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.76;
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.43;
                                                                                                                                BB
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                                                Length
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                                                 1361;
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Best Local Similarity
RESULT 322
ID ADA49171 standard;
DE Maize gene conferri
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
RESULT 326
                                                                                                                                                                                                  Query Mat
Best Loca
RESULT 325
                                                                                                                                                                                                                                    DE PN PA PA
                                                          Best
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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W02003000906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ12052 standard; DI
Maize cDNA modulated
US2003135888-A1.
                                                                                                                                                                                                                                                                                      (BUDW/) BUDWORTH P.
(MOUG/) MOUGHAMER T.
(BRIG/) BRIGGS S P.
(COOP/) COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-2003.
(ZHUT/) ZHU T.
(WANG/) WANG X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYGN ) SYNGENTA PARTICIPATIONS AG
ry Match 2.8%; Score
t Local Similarity 51.1%; Pred.
                            MUZ//1193 standard; DNA; 521 BP.

DNA homologous to phytopathogen resistance-related

WO2003020905-A2.
                                                                                  DNA homologous to phytopathogen WC200320905-A2.
WC20033.
13-WAR-2003.
(DOWC ) DOW CHEM CO.
                                                                                                                                                                       ADQ97220 standard; DNA; 52640 BP.
Mouse cancer associated sequence MD08-015,
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                         ADJ42640 standard;
Plant cDNA #3640.
                                                                                                                                                                                                                                                                                                                                 US2004016025-A1.
                                                                                                                       ADC76479 standard; DNA; 521 BP.
                                                                                                                                       (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.8%;
Local Similarity 57.9%;
                        L3-MAR-2003
                                                                   ocal Similarity
                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                   cal Similarity
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GOFF S A.
KATAGIRI F.
KREPS J.
MOUGHAMER T.
PROVART N.
RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORNELL RES
                                                                                                                                                                                                                           RICKE D.
ZHU T.
                                                                                                                                                                                                                                           KATAGIRI F.
KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHANG H
                                                                                                                                                                                                                                                                    GLAZEBROOK J.
GOFF S A.
                 DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S FOUND IN
2.8%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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51.1%;
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2.8%;
48.5%;
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Pred.
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Pred.
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Pred.
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Pred. No. 1
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 Score
Pred.
                                                                                                                resistance-related
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No. 1.1;
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No. 0.
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No. 0.
                                                                     No.
                                                                                                                                         No
141
 41;
No.
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  DB
1.1;
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..1;
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,9;
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(.7;
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                                                                             10;
          10;
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                                             CDNA
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                                                                                                                                                                                                                       727;
                                                                                                                                                    52640;
                                                                                                                  SEQ
                                             OES
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                                             甘
                                                                                                                  1748
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Best Local Similarity

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RESULT 328
ID ADK570
DE Plant
PN WO2003
PD 13-MAF
PA (DOWC
PA (DOWC
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ID AD
DE P1
PN WC
PD 13
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Best Local S
RESULT 334
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                  Best Local Similarity RESULT 336
                                                                                                     Best Local Similarity RESULT 335
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                                     Query Match
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WO2003020936-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK57003
                                                                                                                                                                                                                                                                                                                                                                                            AAC43155 standard; DNA; 975 BP. Arabidopsis thaliana DNA fragment EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ51912 standard; cDNA; 936 BP.
Aspergillus oryzae polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAAD-) NAT INST ADVANCED IND SCI & (NARE-) NAT RES INST BREWING. (NORQ ) NAT FOOD RES INST MIN AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus ory
WO200279476-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003020936-A1.
                                                                                                            03-JAN-2003.
03-JAN-2003.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
3ry Match
2.8%; Score
2.8%; Pred.
                                                                                                                                                                                                                                        Arabidopsis tha WO200281695-A2.
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
WO200216655-A2.
                                                                                                                                                                                                                                                                                                                                                ABZ14388 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES
                                                                        AAF14569 standard;
Aspergillus oryzae
WO200056762-A2.
                                                                                                                                                     Arabidopsis thal WO2003000898-A1.
                                                                                                                                                                        ADA68286 standard; DNA;
                                                                                                                                                                                                                                                    ABZ42072 standard; cDNA; 975 E
Arabidopsis thaliana gene #56
                                                                                                                                                                                                                                                                             (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS
(SYGN 2.8%; Scc
ry Match 2.8%; Scc
t Local Similarity 48.9%; Pro
                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG (FRIE-) FRIEDRICH MIESCHER INST
Human
 ADJ67514 standard; DNA;
Human ovarian specific (
                                                                 28-SEP-2000
                                              (NOVO ) NOVO
                                                                                                                                                                                          Local Similarity
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NORDISK AS.
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which
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h confers altered
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gene 8
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n confers altered metabolic characteristic
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WO2004013311-A2
12-FEB-200
                                     Bovine embryonic
                                                                                           Murine cancer-associated WO2004058146-A2.
                                              ABN74463 standard;
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Murine cancer-associated (CA) gene
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Plant cDNA #2936.
US2004016025-A1.
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                                                                                                                                                                                                                                                                                                                                   ADR64131 standard;
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ry Match 2.7%;
t Local Similarity 49.8%;
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(ZHOU/) ZHOU Y.
(CAOY/) CAO Y.
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CY Match

Local Similarity 49.8%;
                                                                            SAGR-) SAGRES DISCOVERY INC.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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Similarity
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GOFF S A.
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KATAGIRI F.
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erm (EG) cell
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Best Loca
RESULT 351
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RESULT 347
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                          ADB53373 standard; DNA; 3513 BP. Primary rat hepatocyte toxicity WO200306593-A2.
14-AUG-2003.
                                                                                                               ADB58685 standard; DNA; 3513 I
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Human soft tissue sarcon
                                                                                                                                                                                                                                                             ACA43874 standard; DNA; 2394
Prokaryotic essential gene #:
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                                                                                                                                                                                                                                                                                                                                   ABK63445 standard; cDNA; 654 BP. Rat sequence differentially exp
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"Y Match 2.7%; Sc
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                                                                                       (GENE-) GENE LOGIC
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                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
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2.7%;
Similarity 48.5%;
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h 2.7%;
Similarity 54.4%;
Similarity
                  GENE LOGIC INC.
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gene for cons
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RESULT 359
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RESULT 361
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(FISH/) FISHER D I
(LIUJ/) LIU J.
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(FISH/) FISHER I
(LIUJ/) LIU J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS55208 standard; cDNA; 1278 BP. Calcium sensitive circularly perm
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28-NOV-2002
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Toxicity modelling
DNA homologous t WO2003020905-A2.
                                                                                                                                                                                                                                                                         Maize sucrose synthase US2003135870-A1.
                                                                                         AAA31443 standard; DNA; 350 Plant microsatellite marker
                                                                                                                                                                                                                                                                                                                                                   WO200159063-A2.
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                  ADC77194 standard;
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FLETCHER CHALLENGE FOREST LTD
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48.5%;
        phytopathogen resistance-related
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53.1%;
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57.7%;
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48.1%;
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EST #199.
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ST #209.
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#404.
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polynucleotide
                                     Score 39.8;
Pred. No. 2;
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No.
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No. 1
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No.
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No. 4.
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7.1;
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3.3;
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1.8;
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2.4;
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Best Local Similarity RESULT 367
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RESULT 364
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RESULT 363
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Best Local Similarity
RESULT 362
                             Best Local Similarity RESULT 370
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                                                                                                                    Human secreted protein EP1033401-A2. 06-SEP-2000. (GEST) GENSET.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Rice gene, SEQ II
WO2003000898-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK59087 standard;
                                                                                                                                                                ABT42002 standard;
Toxicity modelling
WO200295000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADA68724 standard;
Rice gene, SEQ ID
ADS55071 standard; cDNA; Bacterial polynucleotide US2003233675-A1.
                                        (SYGN ) SYNGENTA PARTICIPATIONS AG

YMATCH 2.7%; Score

t Local Similarity 50.3%; Pred.
                                                                                Rice gene, SEQ I
WO2003000898-A1.
                                                                                          ADA69683 standard; DNA; 1248 Rice gene, SEQ ID 3006.
                                                                                                                                                                                                        (GENE-) GENE LOGIC INC.

2.7%;

ry Match 2.7%;

t Local Similarity 48.9%;
                                                                                                                                                                                                                                                 Primary rat hepatocyte toxicity modelling WO2003065993-A2
                                                                                                                                                                                                                                                                     ADB52875 standard; DNA; 1139
                                                                                                                                                                                                                                                                                                                        07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC10892 standard; cDNA;
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th 2.7%; Score

l Similarity 50.3%; Pred.
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sequence which confers altered
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AGROSCIENCES
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ID 2047.
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50.3%;
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48.9%;
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h confers altered metabolic
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#7058.
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RESULT 373
ID AAN801
DE DNA er
PN WO8809
PD 01-DEC
PA (CREA-
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DE PA
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Best
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                                                                            ADA48926 standard; DNA; 709 BP. Wheat gene conferring disease r
                                                      US2004016025-A1.
                                                               ADJ41937 standard; cDNA;
Plant cDNA #2937.
                                                                                                                                                                                                                                                                                Plant cDNA #3634.
                                                                                                                                                                                                                                                                                                                                     WO8809344-A.
                                                                                                                                                                                                                                                                                                                                                     AAN80188 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                     Mouse ischaemic
WO200188188-A2.
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US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS49559 standard; cDNA;
                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS AG.
TY Match 2.7%; Score
Local Similarity 49.1%; Pred.
                                                                                                                                                                                                                                                                                      DJ42634 standard;
                                                                                                                                                                                                                                                                                                                                                                    (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

CY Match 2.7%; Score 39.8; I

Local Similarity 49.3%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                     ABI99819 standard;
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             MOUGHAMER T.
BRIGGS S P.
COOPER B.
                            BUDWORTH P.
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SLATER S
CHEN X.
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ZHU T.
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BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                            BUDWORTH P.
BUDWORTH P.
                                                                                                                                                                                     KREPS J.
PROVART N.
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KATAGIRI F.
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h 2.7%; (
Similarity 48.3%; )
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multifunctional
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Score
Pred.
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Pred. No. 8.4;
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RESULT 382
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RESULT 384
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RESULT 383
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Best Local Similarity
RESULT 377
                         Query Match
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                                                ABN80303 standard; DNA; 6120 BP. Human chemically modified disease W0200200927-A2.
                                                                                                                                                                                  ABN80332 standard; DNA; 3001 BP. Human chemically modified disease associated WO200200927-A2.
                                                                                                                 DNA transcription WO200192565-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed WO200171042-A2.
                                                                                                                                  ABK28440 standard;
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ry Match 2.7%; Score
t Local Similarity 45.9%; Pred.
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                                                                                                                                                                                                                                                            Rice gene,
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                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                       ADR46441 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL14119 standard; cDNA;
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KREPS J.
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                                EPIGENOMICS
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               Similarity
standard; DNA; 118063 BP
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2.7%;
61.8%;
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protein c
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Best Local Similarity
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ID AD035602 standard; I
DE Novel mouse gene seg
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ID ADA709
DE Rice 9
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                                                                     ADA70926 standard; DNA; 1146
Rice gene, SEQ ID 4249.
WO2003000898-A1.
                                                                                                                                             AAC50296 standard; DNA; 514 BP. Arabidopsis thaliana DNA fragment EP1033405-A2.
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22-NOV-2001.
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(FIVE-) FIVE PRIME THERAPEUTICS INC.
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        ADJ40264 standard;
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ry Match 2.7%;
t Local Similarity 48.4%;
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(SAGR-) SAGF
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CDNA #1264.
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h 2.6%; Score
Similarity 50.0%; Pred.
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                                           AAV04232 standard; cDNA; 495 B
Human cardiac troponin C cDNA.
W09739132-A1.
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17-APR-2003.
                                                                                                                                                                                                                                ACH18454 standard;
Human adult heart o
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Human adult heart cDNA #1029.
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                                 (SPEC-)
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(LABA/) LABAT I.
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LABA/) LABAT I.
STAC/) STACHE-CRAIN
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GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
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ZHU T.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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standard; cDNA; 795
                                 DIAGNOSTICS
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(SHIQ/) SHI Q.
(SONG/) SONG Q.
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05-NOV-2002.
(SPEC-) SPECTRA
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(SHIQ/) SHI Q.
(SONG/) SONG Q.
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                       WO2004048938-A2.
10-JUN-2004.
                                       ADQ23279 standard; DNA; 1225
Human soft tissue sarcoma-upi
                                                                                                                                                                      Human cardiac WO9931235-A1.
                                                                                                                                                                                                                                      ADE77155 standard; cDNA; 1158 Human cDNA differentially expr
                                                                                                               Human cDNA encoding
                                                                                                                        ADG14205 standard;
                                                                                                                                       (SPEC-) SPECTRAL DIAGNOSTICS ry Match 2.6%; t Local Similarity 51.4%;
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Human cardiac troponin I and
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DNA encoding cardiac troponin I/cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH03848 standard; cDNA; 844 BP.
                 (PROT-)
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               PROTEIN DESIGN LABS
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17-SEP-1998.
17-SEP-1998.
(REGC) UNIV CALIFORNIA.
2-6%;
2-6%;
48.8%;
                                                  AAA31857 standard; DNA; 278 Plant microsatellite marker WO9967421-A1.
                                                                                          ADP74816 standard; DNA; 137560 BP.
Parapoxvirus ovis genome DNA seque
zry Match
$\frac{2.6\$; Score}{1}$
$\text{tocal Similarity} \frac{50.3\$; Pred.}{1}$
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2.6%;
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(REGC) UNIV CALIFORNIA.
PROPERTY Match
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WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS55209 standard; cDNA; 1284 Calcium sensitive circularly EP1238982-A1.
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Human activated T cell cDNA #1
US2002137077-A1.
26-SEP-2002.
                                                                                                                                                                    03-JAN-2002.
(EPIG-) EPIGENOMICS
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Human immune system associated o
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                   (GENE-) GENESIS F
(FLET-) FLETCHER
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(PETE/) PETERSON D
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                    CHALLENGE FOREST LTD
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circularly permuted
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               Human cDNA diffe
US2002160382-A1.
31-OCT-2002.
                                 ADA10931 standard; cDNA; ;
Human cDNA differentially
                                                                                         Bacterial source DNA
WO2004033668-A2
                                                                                                           ADM99174 standard;
                                                                                                                                                                  Human zygote arrest WO2003091400-A2.
                                                                                                                                                                          ADJ63193 standard; DNA; 1275
Human zygote arrest 1 (Zar1)
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                                                                                                                                                                                                                                                    AAF93577 standard;
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                                                                                                                                                                                                                                                                                                            ADD33310 standard; DNA; Mouse mitochondrial DNA
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Toxicity modelling
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                       ACH89551 standard;
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ry Match 2.6%; Score
L Local Similarity 50.0%; Pred.
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Renal cell carcinor
                                   Human cDNA encod US2003073196-A1.
                                                                                                  03-APR-2003.
                                                                                                          Human cDNA encoding US2003064474-A1.
                                                                                                                                                                                                                                                        cDNA encoding human WO200224888-A2.
                                                                                                                                                                                                                                                               ABK70004 standard; DNA; 2945 BP cDNA encoding human Pro peptide
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                                          ADA43552 standard; cDNA; 2945 BP.
Human cDNA encoding secreted/transmembrane
                                                                                                                            ADA43784 standard; cDNA; 2945
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                     Human PRO polynucleotide US200373192-Al. 17-APR-2003.
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                                                                                              ADB66149 standard; cDNA; 2945 BP. Human cDNA encoding secreted/transmembrane US2003082729-A1.
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Human PRO polynucleotide
US2003068781-A1.
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Human PRO polynucleotide
US2003082726-A1.
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Human PRO polynucleotide SEQ 1
US2003082728-A1.
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10-APR-2003.
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US2003068778-A1.
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                                                                                                              ADD95483 standard; cDNA; 2945 BP.
Human cDNA encoding secreted/transmembrane
US2003064473-A1.
03-APR-2003.
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Human PRO28700 cDNI
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ADE38188 standard; cDNA; 2945 BP
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Human PRO polynucleotide #44
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US2003077741-A1.
                                                                      Human cDNA encoding secreted/transmembrane US2003104561-A1.
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05-JUN-2003.
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Human PRO polynucleotide #44.
US2003077742-A1.
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Human cDNA encoding secreted/transmembrane US2003073188-A1.
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Human PRO polynucleotide
US2003073189-A1.
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          ADE37712 standard;
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03-JUL-2003.
(GETH) GENENTECH INC.
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Human PRO polynucleotide #44.
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Human PRO polynucleotide #44.
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     Human cDNA encoding US2003104563-A1.
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                        ADE37480 standard; cDNA; 2945 BP.
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                                      Human cDNA encoding US2003119136-A1.
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Human PRO28700 cDNA.
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Human cDNA encoding secreted/transmembrane
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Novel human secreted and
US2003119128-A1.
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Novel human secreted and
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No. 12;
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Best Local Similarity RESULT 522
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RESULT 523
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                                                                                                                                                                                                                                                                                                                                                Human cancer-associated WO2004035789-A1.
        (FISH/)
(LIUJ/)
                                                                                                                                                                                             ACN45200 standard; DNA; Mouse genomic sequence m WO2003073826-A2.
                                                                                                                                                                                                                                                                               ADJ63204 standard; DNA; 6002
Human zygote arrest 1 (Zar1)
WQ2003091400-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM12925 standard; cDNA; 2945 PRO28700 encoding sequence. WO2004024077-A2.
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                                            Maize sucrose sy US2003135870-A1.
                                                                                                                   Human secreted EP1033401-A2.
                                                                                                                            AAC23266 standard; cDNA; 214 BP.
Human secreted protein 5' EST, SEQ
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WO2004028479-A2.
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                                                                                                   (GEST ) GENSET.
                                                                                                            06-SEP-2000
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ry Match
2.6%;
Local Similarity 58.1%;
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       CHEIKH N. FISHER D :
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                                                     synthase
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58.1%;
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g secreted/transmembrane
                                                               cDNA; 233
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58.1%;
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protein
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#44.
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No. 14;
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No. 12;
38.4;
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No.
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233;
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(FISH/) FISHER D
(LIUJ/) LIU J.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
ADA58895 standard; cDNA; 383
                                     (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                      ADA58904 standard; cDNA; 360 BP.
Maize sucrose synthase EST #548.
                                                                                                                                      (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                  ADA58410 standard;
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                              US2003135870-A1.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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(FISH/) FISHER D
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ST #54.
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#273.
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#136.
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#179.
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No. 4.
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                   38.4;
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No. 4.
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No. 4.3;
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No. 4.
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Best Loc
RESULT 538
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Best Local Similarity
RESULT 537
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RESULT 535
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RESULT 540
Best Local Similarity RESULT 541
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17.JUL-2003.
(CHEI/) CHEIKH N.
(FISH/) FISHER D F
(LIUJ/) LIU J.
                                                                                                                                                                                         (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                               ADA58909 standard; cDNA; 413
Maize sucrose synthase EST #5
US2003135870-A1.
17-JUL-2003.
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                                                                                                                                ABN95419 standard;
Gene #1917 used to
WO200229103-A2.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant cDNA #2964.
US2004016025-A1.
                            ADA03007 standard; cDNA; 450 BP.
Mouse Calm2 carcinoma associated
W02003057146-A2.
17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                          ADA58893 standard; cDNA
Maize sucrose synthase
US2003135870-A1.
17-JUL-2003.
                                                                                                                                                                                                                                                                                             (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                             Maize sucrose sy US2003135870-A1. 17-JUL-2003.
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(BRIG/)
(COOP/)
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                                                                                                             (GENE-) GENE LOGIC
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KREPS J.
PROVART N.
RICKE D.
ZHU T.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
                                                                                                                                                                                                                                                                                                                                                synthase EST
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2.6%;
52.9%;
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diagnose
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52.5%;
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EST #537.
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55 %
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#519.
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#553.
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Pred.
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Pred. No. 5.
            Score 38.4;
Pred. No. 5
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No. 5.
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No. 5.
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No. 5.
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                                                                                                                                                                                      Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 392;
                                                               SEQ ID NO:1525
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CDNA;

450

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PA PRO PA
                      Query Match
Best Local Similarity
RESULT 549
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Plant DNA sequence WO2003020936-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                            ADM74602 standard; DNA; 450 Murine carcinoma associated
                ADK56992 standard;
                                                              WO2003020905-A2.
                                                                     DNA homologous to
                                                                            ADC75913 standard;
                                                                                                                           DNA homologous to WO2003020905-A2.
                                                                                                                                          ADC77182 standard;
                                                                                                                                                                                       Human ovarian antigen WO200200677-A1.
                                                                                                                                                                                                       ABQ55780 standard;
                                                                                                                                                                                                                                                                     Maize sucrose synthase
US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                  US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                        Maize sucrose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                       US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Calm2 coding WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC85487 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72745 standard;
Mouse Calm2 cDNA.
                                                                                                                                                                                                                                                                                                                  (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003008583-A2
                                                                                                                                                                                                                                     (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                 NDA58866 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                               (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
                                              DOWC ) DOW CHEM CO
                                                                                                                                                                                                                                                                                    DA58877 standard; cDNA;
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                                                                                                     Match
                                                                                            ocal Similarity
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h 2.6%;
Similarity 49.0%;
                                                                                                            DOW CHEM CO
                                                                    ; DNA; 595 BP.
phytopathogen resistance-related
                                                                                                                                 ; DNA; 595 BP.
phytopathogen resistance-related
                DNA;
                                                                                                                                                                                                cDNA; 591 |
gen HOPKG47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
        which
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2.6%;
49.3%;
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49.0%;
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52.5%;
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EST #5
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No. 6.
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        metabolic characteristic #4375.
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Query Match
Best Local &
RESULT 550
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RESULT 557
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Soybean calmodulin-5 cDNA.
1 EP101853-A1.
2 12-JUL-2000.
A (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
A (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
2.6%; Score 38.4; D:
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13-MAR-2003.
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                                                                                                                                                                                                                                                                                                           ABA16488 standard; DN Human nervous system WO200159063-A2.
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16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
2.6%;
2.5%;
2.5%;
                                                                                                                                                      Mouse genomic se
WO2003073826-A2.
 ADA58496
                                                                          Maize sucrose sy US2003135870-A1.
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WO2003073826-A2.
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WO200159063-A2.
                                    (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                              ADA58523 standard; cDNA;
                                                                                                                                                                                                                                                     ACN45034 standard; DNA; 99588
                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA16489 standard;
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                                                                                                                                  (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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h 2.6%;
Similarity 56.2%;
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standard; cDNA; 288
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                                                                                   synthase
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em related
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em related
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48.6%;
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48.6%;
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56.9%;
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42.1%;
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52.5%;
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h confers
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#167.
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polynucleotide
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No. 18;
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No. 6.3;
                   38.2;
No. 4
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No. 8
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No. 15;
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                             281;
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ADS49594 standard; cDNA; Bacterial polynucleotide US2003233675-A1.
                                                                                                                                                                                                                  ADJ42633 standard;
Plant cDNA #3633.
US2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                              US2003194704-A1.
16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                             ACH87297 standard; DNA; 603
Human genome derived single
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                                                                                  AAQ99367 standard;
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                                                (CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA58458 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                   (RANK/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHBI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                            (MOUG/)
(BRIG/)
(COOP/)
                                                                                                                                                                                                                                                                   HYSE-) HYSEQ INC.
                               Local Similarity
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GOFF S A.
KATAGIRI F.
                                                                                                                                                                           BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                  KREPS J.
PROVART N.
                                                                                                                   ZHU T.
                                                                                                                          RICKE D.
                                                                         : DNA; 179
                                                                                                                                                                                                                                    CDNA; 800
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SEQ ID NO: 30368.
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5-10 gene.
        2313 BP. #4337.
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#102.
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3.3;
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Query Match
Query Match
Best Local Similarity
RESULT 566
ID ADSESSOR
Query Match
Best Local S
RESULT 573
ID ADX14120
DE Human aut
PN US2003228
PD 11-DEC-20
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RESULT 568
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Best Local Similarity
RESULT 571
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA23764 standard; DNA; 2421 BP. prokaryotic essential gene #5421. WO200277183 -A2. 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial polymucleotide #7092. US2003233675-A1.
          ADK14120 standard; cDNA; 4
Human autoimmune disorder
US2003228617-A1.
                                                                                                                                                                                                                                                  Human src biomar WO2003062395-A2.
                                                                                                                                                                                                                                                                                                                               Hypoxia-induced protein WO200246465-A2.
                                                                                       ADP24081 standard; cDNA; PRO polypeptide encoding WC2004041170-A2.
                                                                                                                                                                     Antipsoriatic cDNA
WO2004028479-A2.
                                                                                                                                                                                        ADN04316 standard;
                                                                                                                                                                                                                                                                       ADD14797 standard;
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                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                     GETH ) GENENTECH INC.
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SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEN X.
GOLDMAN B
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                                                 Similarity
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sequence #358.
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polynucleotide
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No. 17;
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  뭐당
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                                                                         AAS74660 standard;
DNA encoding novel
WO200175067-A2.
                                                                                                                                                                                                                                                                       AAA31969 standard; DNA; 345 Plant microsatellite marker WO9967421-A1.
                                                                                                                                                                                                                                                                                                                                                             ACN44936 standard; DNA; 50460 BP. Mouse genomic sequence mCG5738. WO2003073826-A2.
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AAA31454 standard; DNA; 404 Plant microsatellite marker
                                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FOREST LTD.
TY Match 2.6%; Score 38;
Local Similarity 49.0%; Pred. No.
                                                                                                                                                                         Plant microsatellite WO9967421-A1.
                                                                                                                                                                                               AAA31680 standard;
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(FLET-) FLETCHER CHALLENGE FOREST L
TY Match 2.6%; Score
L Local Similarity 49.0%; Pred.
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WO2003091400-A2.
06-NOV-2003.
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Human zygote arrest 1 (?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
ry Match 2.6%; Score 38.2;
t Local Similarity 49.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cervical cancer marker nucleic acid 4574.
WO200142467-A2.
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ry Match 2.6%;
Local Similarity 54.7%;
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                                                     HYSE-) HYSEQ INC
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te marker
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                                                                                   cDNA; 381 BP.
human diagnostic
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49.8%;
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56.3%;
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nucleotide sequence
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#641.
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#930.
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Pred. No.
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SEQ ID NO:2458
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No. 25;
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RESULT 590
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Best Local Similarity
RESULT 583
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Zea mays DNA fragment SEQ ID NO: 30519
EP1033405-A2.
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Variable Res Inst.

(SCRI) SCRIPPS RES INST.

(SYGN) SYNGENTA PARTICIPATIONS AG.

(SYGN) SYNGENTA PARTICIPATIONS AG.

48.6% Pred.
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(GENE-) GENESIS RES & DEV C
(FLET-) FLETCHER CHALLENGE
                                                         ADC77186 standard; DNA; 617 DNA homologous to phytopatho WC2003020905-A2.
                                                                                                                                                                                                                                    WO2003020905-A2.
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ADK56996 standard; DNA; 617
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Plant DNA sequence which confers altered metabolic
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Arabidopsis thaliana DNA fragment
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W02003000898-A1.
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                                        (DOWC )
                                                                                                                       (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
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h 2.6%; Score 38;
Similarity 48.6%; Pred. No.
                                      DOW CHEM CO.
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phytopathogen
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phytopathogen
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RESULT 592
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PN US2001
PN (GORT)
PA (HAMI)
PA (PARIC)
PA (RAIN)
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RESULT 595
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Kidney cancer related
WO200194629-A2.
                                                       Lung cancer related gene WO200194629-A2.
                                                                                             ABL66947 standard; DNA; 62944 BP
                                                                                                                                                                                                                                                                                                                                                               ADJ57067 standard;
Vector plasmid pEE
WO2004009823-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA10594 standard; DNA;
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2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS
                                                                                                                                                                        (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OJIP ) OJI PAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (/YYWA
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ALLEN K.

HOFFMAN N.

HURBAN P.
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MATHEW A V.

LEDFORD B L.

WOESSNER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
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DOW AGROSCIENCES LLC.
                   AVALON PHARM.
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15.1 hCMV/GFP+hot
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2.6%;
51.8%;
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13.8%;
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 2.6%;
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of cellulose
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                                                                         sequence
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Best Local Similarity
RESULT 605
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US2003073623-A1.
17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse cancer-associated WO2004074320-A2.
                                                                                                                       ACH28432 standard; cDNA; 455
Human adult ovary cDNA #6812
US2003073623-A1.
          ACH17443 standard; cDNA; 459 BP.
Human adult heart cDNA #1757.
                                                                                                                                                                                                                                                                                                                                                                        Human adult heart
US2003073623-A1.
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Murine cancer-associated (CA) gene
US2003073623-A1.
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Human adult heart cDNA #2551.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
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(SAGR-) SAG
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) LABAT I.
) STACHE-CRAIN I
) DICKSON M C.
) JONES L W.
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DICKSON M C.
JONES L W.
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                                                           JONES L W.
                                                                     STACHE-CRAIN
DICKSON M C.
                                                                                                                                                                                                                                                                                       Similarity
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LABAT I.
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49.3%;
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56.3%;
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No. 7.
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1.1e+02;
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L7-APR-2003

DRMANAC R T. LABAT I.

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Query Match
Best Local Similarity
RESULT 612
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Best Local Similarity
RESULT 607
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                           ACN40763 standard;
Tumour-associated;
WO2004030615-A2.
ADJ56207 standard; cDNA; 1
Human cDNA differentially
US2003119009-A1.
                                                                  Human polynucleotide WO200164835-A2.
                                                                                   AAI93806 standard;
                                                                                                                                    WO200166689-A2.
                                                                                                                                             cDNA encoding novel
                                                                                                                                                      AAS45021 standard;
                                                                                                                                                                                                        Respiratory disease WO2003101283-A2.
                                                                                                                                                                                                                          ADK70382 standard;
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Human differential transcription-associated
W0200157058-A2.
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Human adult heart cDNA #386.
US2003073623-A1.
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                                                 HYSE-) HYSEQ INC.
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                                 ocal Similarity
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LABAT I.
STACHE-CRAIN
DICKSON M C.
JONES L W.
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DICKSON M C.
JONES L W.
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                                                                                                                   HYSEQ INC.
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                                                                                                                                                                                                                                                                                  l; cDNA; 111
l antigenic
                                                                          cDNA; 1306 BP.
de SEQ ID NO 13866.
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2.5%; Score |
49.3%; Pred. |
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Herry N.
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RESULT 614
ID ACA
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RESULT
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RESULT 617
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ESULT 620
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30-JUL-2002.
(CYTO-) CYTOKINETICS INC.
(CYTO-) CYTOKINETICS INC.
2.5%;
ery Match 2.5%;
44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene #7950. WO200277183-A2. 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2003.
(STUA/) STUA
(NUCH/) NUCH
(PLON/) PLON
                                                               ACC47237 standard; cDNA; 5197 BP.
Human SCAP encoding cDNA-Incyte Id.
WC2003008625-A2.
                                                                                                                                                           Human kinesin-like
US6455293-B1.
                                                                                                                                                                                                        (CYTO-) CYTOKINETICS INC.
Pry Match 2.5%;
It Local Similarity 44.0%;
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WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
(ELIT-) ELITRA PHARM INC.
2.5%;
ry Match
2.5%;
t Local Similarity 52.2%;
                                                                                                                                                                      ABS57218 standard; DNA; 4911
Human kinesin-like protein, !
                                                                                                                                                                                                                                          US6383796-B1.
07-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                          ABQ81185 standard; cDNA; 491
Human kinesin motor protein
                                                                                                                                                                                                                                                                                                                                                                                            (CNRS ) CENT NAT RECH SCI.
ry Match 2.5%;
t:Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EP600136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ65476 standard;
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US2003099974-A1.
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XY Match 2.5%; Score

t Local Similarity 50.3%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA71195 standard; DNA; 1839 Rice gene, SEQ ID 4518.
ABX11086 standard; DNA; 42999
                                              (INCY-)
                                                                                                                                                                                                                                                                             ABK52651 standard;
                                                                                                                                                                                                                                                                                                                                                US6426193-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta-3
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ry Match 2.5%;
t Local Similarity 49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN90405 standard;
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                                                                                                                                     (CYTO-) CYTOKINETICS
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) NUCHTERN J G
) PLON S E.
) SHOHET J M.
                      Similarity
                                             INCYTE
                                                                                                                                                                                                                                                                 ndard; DNA; 4911 BP.
human kinesin motor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ndard; DNA;
adrenergic
                     E GENOMICS INC.
2.5%;
arity 44.0%;
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related marker,
                                                                                                              CS INC.
2.5%;
44.0%;
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49.3%;
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ein HsKif21b
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No. 16;
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No. 14
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No. 26;
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No. 26;
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No. 22;
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No.
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(rrna)

gene

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Best
RESULT
                                                                  Best Local Similarity
RESULT 630
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RESULT 623
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                                                Plant DNA sequence
                                                                                                                         Plant DNA sequence WO2003020936-A1.
                                                                                                                                                                                                   ADC75911 standard; DNA; 526 BP. DNA homologous to phytopathogen WO2003020905-A2.
                                                                                                                                                                                                                                                                    ADC77195 standard; DNA; 526 BP. DNA homologous to phytopathogen WO2003020905-A2.
                                                                                                                                                                                                                                                                                                                                                                         Murine carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC85413 standard;
Mouse Braf genomic
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Mouse Braf gene.
WO2003008583-A2.
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                                                                                                                                            ADK57005 standard;
                                                         NDK55189 standard;
                                                                                                                                                                               13-MAR-2003.
(DOWC ) DOW CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                 US2004072154-A1.
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(SAGR-) 2.5%;
ry Match 2.5%;
t Local Similarity 54.7%;
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                                                                                                                                                                                                                                                                                                                                    (MORR/) MORRIS D W. (ENGE/) ENGELHARD E
                                                                                                                                                                                                                                                                                                                                                                                  ADM74528 standard; DNA; 96599
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TY Match 2.5%;
Local Similarity 54.7%;
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DOW AGROSCIENCES LLC.
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2.5%;
Similarity 54.7%;
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54.7%;
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No. 9.
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No. 9.
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No. 78;
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No. 9.
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No. 1.
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.2e+02;
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.2e+02;
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.2e+02;
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Query

Score

37.6;

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Best Local Similarity
RESULT 639
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RESULT 636
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Best Local Similarity
RESULT 635
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RESULT 634
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RESULT 633
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RESULT 632
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US6551795-B1
22-APR-2003.
                                                                                                                                                                                                                                                    Pseudomonas aeruginosa polynucleotide #5181.
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa F
US6551705-51
Human Jagged 2 I
US2003170636-A1
                                                                                  ADD00948 standard; cDNA;
Human Jagged 2 encoding woo2003077848-A2.
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"YY Match 2.5%;

It Local Similarity 49.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA clone originating in WO2003057877-A1.
                    ADH62908 standard;
                                                              25-SEP-2003.
(ISIS-) ISIS
                                                                                                                                                  (GENO-)
                                                                                                                                                                                          ABD06690 standard;
                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS ry Match 2.5%; t Local Similarity 51.2%;
                                                                                                                                                                                                                                              22-APR-2003
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US2003233675-A1.
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"YY Match 2.5%;

"t Local Similarity 49.0%;
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2.5%; Scor
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ry Match 2.5%;
t Local Similarity 49.0%;
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aeruginosa polynucleotide
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           DNA;
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                                         2.5%;
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polynucleotide
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cDNA 8
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n barley
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barley
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                                                                                                                                                       ADR73469 standard;
Human jagged 2, JAC
WO2004076682-A2.
                                                                                                                                                                                                                                                                                                                                                                         ADH57070 standard; DNA; DNA of a human Jagged 2 US2003207839-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD00955 standard; cDNA; 4974
Human Jagged 2 encoding cDNA;
WO2003077848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA of a human Jagged US2003207839-A1.
WC2004074320-A2.
                 Mouse cancer-associated genomic DNA MD12-017
                                                                                 WO2004074320-A2.
                                                                                        ABD32870 standard; DNA;
Mouse cancer-associated
                                                                                                                                                                                                                                ADR83400 standard;
Human jagged 2 DNA,
WO2004076622-A2
                                                                                                                                                                                                                                                                                                        ADN03615 standard; cDNA; 5077
Antipsoriatic cDNA sequence #1
W02004028479-A2.
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Human Jagged 2 DNA
US2003170636-A1.
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                           ABD32610 standard; DNA;
                                                                                                                                                                                            (NAAD-) NAT INST ADVANCED IND 2.5%; sty Match 2.5%; st Local Similarity 52.6%; st
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                                                                                                                                      (SURR-) SURROMED
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                                                              SAGRES DISCOVERY INC.
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52.6%;
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genomic DNA MD17-083
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9 37.6; DB 13;
NO. 31;
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No. 31;
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No. 31;
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No. 30;
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Best Local Similarity
RESULT 649
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RESULT 654
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Best Local Similarity
RESULT 656
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RESULT 651
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07-AUG-2003.
(GENE-) GENE LOGIC INC.
2.5%;
Ammin Match 2.5%;
47.0%;
                                                                                                                                                                                                                                                                                                                                         Primary rat hepatocyte to WO2003065993-A2.
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
2.5%;
ery Match 2.5%;
46.0%;
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                                                                                                                                                                                                                                                  ADB68842 standard; DNA; 536 BP. Minority luxi consensus sequence WC200305790Z-A2.
17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003.
(KANS-) KANSAI TECHNOLOGY LICENSING
ACL19199 standard; DNA; DNA clone originating in WO2003057877-A1.
                                        (UYNI-) UNIV JAPAN OKAYAMA.
ry Match 2.5%;
t Local Similarity 49.2%;
                                                                                             ACL19219 standard; DNA; 593 BP. DNA clone originating in barley
                                                                                                                             (UYNI-) UNIV JAPAN OKAYAMA.

ry Match
t Local Similarity 49.2%;
                                                                                                                                                                        DNA clone originating WO2003057877-A1.
                                                                                                                                                                                               ACL19217 standard;
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Human genomic sequence l
WO2003073826-A2.
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(GENE-) GENE LOGIC
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(APPA/) APPARSUNDARAM S.
(FERG/) FERGUSON S.
                                                                                                                                                                                                                  local Similarity
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2.5%;

Similarity 13.4%;
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58.6%;
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toxicity modelling
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hCG17361.
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In barley
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          593 BP.
barley
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No. 11;
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No. 12;
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No. 12;
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No. 2.1e+02;
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1.8e+02;
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           #9190
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RESULT 666
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RESULT 658
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Best Local Similarity
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                                                                            DNA clone originating in WO2003057877-A1.
DNA clone originating in barley containing WO2003057877-A1.
                                                                                                                                                                                                                                    ACL19205 standard; DNA clone originating WO2003057877-A1.
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17-JUL-2003.
(UYNI-) UNIV JAPAN OKAYAMA.
2:S*;
2:TY Match 2:5*;
49.2*;
                           ACL19216 standard;
                                                                                                                                                             DNA clone originating WO2003057877-A1.
                                                                                                                                                                               ACL19221 standard;
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I7-JUL-2003.
(UYNI-) UNIV JAPAN OKAYAMA.
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ery Match 2.5%;
49.2%;
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(UYNI-) UNIV JAPAN
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                                                                (UYNI-) UNIV JAPAN
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ry Match 2.5%;
t Local Similarity 49.2%;
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ry Match 2.5%;
t Local Similarity 49.2%;
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2.5%;
49.2%;
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2.5%;
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ing in barley
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2.5%;
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n barley
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No. 13;
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Best Local Similarity
RESULT 667
ID ACTION
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RESULT 671
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RESULT
ID AC
                          Best Local Similarity RESULT 674
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RESULT 673
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                                                                                                                                                                                            Query Match
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                                                                                                                                              Human HIPHUM GB2365432-A.
                                                                              ADQ63696 standard; cDNA; 2336 BP Novel human cDNA sequence #857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP29084 standard; DNA; 1044 BP. Human secreted protein encoding WO2004035732-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA clone originating in barley W02003057877-A1.
                                                                       EP1440981-A2.
                                                                                                                                                                                                                      ABX72264 standard; cDNA; i
Human NOVX polynucleotide
WOZ00281498-A2.
Human neurotransmitter transporter
WO2003059947-A1.
                  ACF79238 standard;
                                                                                                                              (GLAX )
                                                                                                                                                                 AAD34007 standard;
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                                                     (REAS-)
                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                               (PROV,
                                                                                                                                                                                                                                                                                                                                           (BRIG/)
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                                                                                                                                                                                                                                                                                                                                                                                                         ADJ39564 standard;
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ry Match 2.5%;
t Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA clone origin WO2003057877-A1.
                                                                                                                                                                                                                                                                              (/IUHZ
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                             GLAXO
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KATAGIRI F.
KREPS J.
                                                     RES
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                                                                                                                                                                                                                                                                                              KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 696 BP. originating in barley
                                 ASSOC BIOTECHNOLOGY.
2.5%; Sco
ilarity 53.8%; Pre
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2.5%; Sco
47.6%; Pre
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2.5%;
49.2%;
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2.5%;
49.2%;
                  CDNA; 2388 BP
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leotide #95.
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47.6%;
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No. 23;
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No. 13;
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No. 13;
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No. 13
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RESULT
ID AB
DE Ps
PN US
PN 22
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Best Local Similarity 49.0%;
RESULT 681
ID ABD17057 standard; DNA; 864
ID ABD17057 standard; DNA; 864
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                               RESULT
  PRE
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RESULT 675
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Best Local
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Best
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SULT 682
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                                                                                ABD17123 standard; DNA; 1428 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                               AAC56719 standard;
Eucalyptus grandis
WO200053724-A2
ABK92063 standard;
DNA encoding novel
WO200229058-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           MOD97161 standard; DNA; 107432 BE MOUBE cancer associated sequence WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC43635 standard; DNA; 2490 BP. Nucleotide sequence of the human FR2828208-A1.
                                                                                                                                                                   Pseudomonas aeruginosa
US6551795-B1.
                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD. (GLET-) FLETCHER CHALLENGE FORESTS LTD. FY MATCh 2.5% Score 37.2; LOCAl Similarity 49.0%; Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                        AAI84688 standard;
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                                       (GENO-) GENOME THERAPEUTICS 2.5%; Local Similarity 44.7%;
                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY INC.
ry Match
Local Similarity 55.9%;
                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                         2-APR-2003
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th 2.5%; Scor

Similarity 44.7%; Pred
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de SEQ ID N
         DNA; 1782 BP.
transmembrane
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47.6%;
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polynucleotide
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                                        37.2; No. 21;
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No. 12;
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No. 24;
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No. 1.
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No. 24;
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No. 24;
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Best Local Similarity RESULT 684
     Query Match
Best Local Similarity
RESULT 687
                                      RESULT 686
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Human NOVX protein Nov45D
US2004014053-A1.
ABD17019
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Human NOV45d gene SEQ II
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                                                                                                                                                                                                                                                                                                                                                                      ADH41902 standard; DNA; 1881 BP.
Novel human nucleic acid NOV36f.
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18-SEP-2003.
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ANDERSON D W.
SPYTEK K A.
GERLACH V.
BURGESS C E.
KHRAMTSOV N V.
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) CASMAN S J.
VOSS B Z.
'LDOG F L.
'GARU M.
'ON G.
                       TAUPIER R
CATTERTON
SHENOY S G
                                                                                     RASTELLI L.
AGRE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
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VERNET C !
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MILLER C E
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gene ε
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            Score 37.2;
Pred. No. 24;
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                   1881;
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Query Match
Best Local S
RESULT 691
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RESULT 694
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Best Local Similarity
RESULT 690
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RESULT 688
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
SETY Match
2.5%; Score 3
SIMILARITY 50.6%; Pred. 1
                                 12-SEP-2003.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
2:5%;
2:TY Match 2:5%;
53:4%;
                                                                                                                                                                                                            Human CYP1A2 gene SEQ ID NO:76. WO2003014387-A2.
                                                                                                                                                                                                                                                                                            Murine cancer-associated (CA) W0200405816er-2.
                                                                                                                        Human secreted protein gene sequence, sry Match 2.5%; Score 37. t Local Similarity 48.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human musculoskeletal system WO200155367-A1.
Maize sucrose synthase EST
US2003135870-A1.
                    ADA58478 standard;
                                                                              ACN45182 standard; DNA; 261817 E Human genomic sequence hCG14925. WO2003073826-A2.
                                                                                                                                                     AAL51405 standard; DNA; 80959 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding novel US2002147140-A1. 10-OCT-2002.
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15-JAN-2004.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
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7.2; DB 8;
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(CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
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Prokaryotic essential ge
WO200277183-A2.
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17-JUL-2003.
(UYNI-) UNIV JAPAN OKAYAMA.
(UYNI-) CONTROL 2.5%;
ery Match 2.5%;
48.7%;
                                                              US6551795-B1.
22-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC43517 standard; DNA; 549 PAC43517 standard; DNA fragment SEQ ID EP1033405-A2.
  Nucleotide sequence
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ry Match 2.5%;

t Local Similarity 53.9%;
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WO2004072281-A1.
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             AAF85145
                                                                               Pseudomonas aeruginosa polynucleotide
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US6551795-B1
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                                                    (GENO-)
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standard; DNA; 1800 BP.
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Best Local Similarity

52.2%;

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Query Match
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03-MAY-2001.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
2.5% Score 37; DB 4; Li
                                                                                                                                                                                                                                   ADM80676 standard; DNA; 46374 BP. Human USH3A gene genomic sequence WO2001097695-A1
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(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX (HUMA-) HUMAN GENOME SCI INC.
                             Human kinase genomic US2003175927-A1.
                                      ADJ37690 standard; DNA; 9 Human kinase genomic DNA.
                                                                                                                                                ABS52847 standard; DNA; 90541 BP.
Human SR protein-specific kinase 2, SRPK2, genomic US200209450-A1.
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WO9843478-A1
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                     (ABUT/) ABU-THREIDEH (GONG/) GONG F.
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h 2.5%;
Similarity 57.3%;
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         APPLERA CORP.
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1.9e+02;
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                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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Best Loca
RESULT 715
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RESULT 717
  Best Loc
RESULT 719
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Best Local Similarity
RESULT 716
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                                                                                                                                                                                       Human genome derived s
US2003194704-A1.
16-OCT-2003.
(PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                  (PENN/) PENN S (
(RANK/) RANK D F
(HANZ/) HANZEL I
                                                                                                                                                                                                                                                                                                                                                                                  AAC36202 standard; DNA; SArabidopsis thaliana DNA EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize sucrose synthase EST #326. US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR31219 standard;
Human SRPK2 kinase
US2004157297-A1.
                                                                                                                                                                                                                                                                                                                    ACH78156 standard; DNA;
Human genome derived sir
US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence WO200151659-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH88704 standard;
                                    (MATH/
                                                                                                                                     US2002059663-A1.
                                                                                                                                              Arabidopsis thaliana polynucleotide SEQ ID NO
                                                                                                                                                      ABQ66069 standard; DNA; 636
                                                                                                                                                                                                                                               ACH78575 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APPL-) APPLERA CORP.
                                                                                                             (/YYYA
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                       ocal Similarity
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) RANK D R.
) HANZEL D K.
PAGE A.

PAGE A.

MATHEW A V.

LEDFORD B L.

WOBS W D.

HANS W D.

GARCIA C A.

KRICKER M.
                                                                               PRICE J L.
RAINES T M.
                                                                                                 HAMILTON C M.
                                                                                                                   GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 16
SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 905
protein
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52.2%;
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50.6%;
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39.7%;
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A fragment
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ID 544.
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No. 16;
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No. 1;
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No.
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1.9e+02;
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2.5e+02;
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Best Local Similarity RESULT 726
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Best Local Similarity
RESULT 722
                                                                                                                  RESULT 728
                                                                                                                                                                                                                                                                                                                                             RESULT 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa polynucleotide US6551795-B1.
ABL68609 standard;
Kidney cancer relat
WO200194629-A2.
                                                                                            AAT62440 standard;
Human L5/3 growth
                                                                                                                           CHILL-) CHILDRENS HOSPITAL MEDICAL
ry Match 2.5%; Score
t Local Similarity 55.5%; Pred.
                                                                                                                                                                              AAQ79728 standard; DNA; 6100
Human L5/3 tumour suppressor
                                                                                                                                                                                                                                                                                                           ABL06732 standard; cDNA; 4298 BP. Drosophila melanogaster expressed W0200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         ABD03441 standard; DNA; 2946 BP.
Pseudomonas aeruginosa polynucleotide #2045.
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(PEKE) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2001037484-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD03306 standard;
                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS 2.5%; t Local Similarity 54.4%;
                                                             (CHIL-) CHILDREN'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF82218 standard;
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                                         Local Similarity
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) DAVIS K R.
) ALLEN K.
) HOFFMAN N.
) HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        IBARAKI PREFECTURE.
h 2.5%;
Similarity 49.5%;
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          dard; DNA; 9980 BP.
related gene sequence
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                                                                                            factor
                                                              HOSPITAL
                                        55.2
                                                                                                                                                                                                                                                                   2.5%;
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                                                                                          6100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2796
gene
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                                        L MEDICAL CENT.
; Score 36.8; I
; Pred. No. 56;
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Pred.
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Pred.
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promoter-related
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Pred.
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re 36.8; DB
d. No. 51;
                                                                                            sequence
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                                                                                                                           CENT.
36.8;
No. 56;
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No. 39;
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No. 38;
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No. 47;
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No. 21;
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           NO:6946.
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Best Loc
RESULT 732
                                              Best Local Similarity RESULT 739
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RESULT 738
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RESULT 733
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Best Local Similarity
RESULT 730
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11-APR-2002
(GENE-) GENE LOGIC INC.
(3-+ch ---++y 55.5%;
DE10127572-A1.
05-DEC-2002.
(PATH-
                                                                                                                                                                                                                                                     Hypermethylation site in human US2003129602-A1.
                                                                                                                                                                               Hypermethylation US6605432-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinase
                           ACA64924 standard; DNA; 201239
Human PLZF DNA corresponding to
                                                                                                WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DARW-) DARWIN DISCOVERY LTD.
PRICE 2.5%;
It Local Similarity 69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN96855 standard; DNA; 9980
Gene #3353 used to diagnose
                                                                                                         Human cDNA differentially
                                                                                                                                                                                                  ADI37256 standard; DNA; 118067
                                                                                                                                                                                                                                                                                                                                                                                                                  ADD15783 standard; DNA; 64467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD50739 standard; DNA; 64467 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-2000
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Murine TGF-beta binding protein (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVAL-)
                                                                             (GENE-) GENE LOGIC
                                                                                                                    ABK83562 standard;
                                                                                                                                                                                                                                          (HUAN/) HUANG T H.
                                                                                                                                                                                                                                                                                                                                    ADP45591 standard; DNA; 92500 BP.
                                                                                                                                                                                                                                                                                                                                                                                              US6582946-B1.
                                                                                                                                                                                                                                                                                                                                                                                                         Human MEK kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACH00100 standard; DNA; 64467 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                   intercellular adhesion
cch 2.5%;
al Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    protein genomic 2.5%; larity 56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                        subfamily
                                                                              INC.
                                                                                                                     cDNA;
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56.7%;
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                                                        2.5%;
58.0%;
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55.5%;
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56.7%;
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55.5%;
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Y expressed
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liver cancer.
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Pred.
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Pred.
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Pred.
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Score
Pred.
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Pred. No. 1.8e+02;
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BC) locus-37.
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breast
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No. 2.
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No.
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2
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1.
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                                                                                                                                        DB 12;
.4e+02;
                                                                                                                                                                                                                        DB 12;
.4e+02;
                                                         DB 6;
.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
.4e+02;
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                                                                   Length 139904;
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GMBH.

Score

36

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BB

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RESULT 746
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RESULT 743
          PAPRE
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Best Local
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                           Nucleotide sequence WO200146387-A1.
                                                                                                                                                                                                                                                                                                                                                       ADA48906 standard; DNA; 689 BP. Wheat gene conferring disease r w02003000906-A2.
                                             AAH74539 standard;
                                                                                                                                                                                                            ADJ41713 standard; cDNA; 689
Plant cDNA #2713.
                                                                                                                                                                                                                                                                                       Wheat DNA sequence
                                                                                                                                                                                                                                                                                                ADC08648 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX52791 standard; cDNA; 438 BP. Bovine EST associated with lactation/muscle/fat deposition #2720. US2002137160-A1. 26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize sucrose synthase US2003135870-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHBI/) CHBIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize вистове
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA58461 standard;
                                                                                                                                                                                                   JS2004016025-A1.
                                                                                                                                                                                                                                                                                                                  (SYGN ) SYNGENTA PARTICIPATIONS AG

ry Match 2.5%; Score

L Local Similarity 49.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003135870-A1.
                                                                                                                                                                                                                                      (SYGN ) SYNGENTA PARTICIPATIONS AG.

TY Match

2.5%; Score 36.6;
Local Similarity

49.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .7-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DA58383 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  BYAT/) BYATT J C.
MATHIALAGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                      -JAN-2003
                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                        BUDWORTH P.

MOUGHAMER T.

BRIGGS S P.

COOPER B.

GLAZEBROOK J.
                                                                                  RICKE D.
ZHU T.
                                                                                                    FROVART N.
                                                                                                                                                                                                                                                                                                                                                                                                               TAO N.
WARREN W C.
                                                                                                                        GOFF S A.
KATAGIRI F.
        CORNELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthase
         RES
                                    cDNA;
e of a
                                                                                                                                                                                                                                                                                      DNA; 689 BP.
Seq ID953 related to grain
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2.5%; Score 36.6;
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49.7%;
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49.7%;
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46.9%;
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56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 340 BP.
EST #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 295 BP.
EST #105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .18;
                                    905 BP.
chitobiosidase
                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                             Score 36.6;
Pred. No. 17;
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Pred.
                                                                                                                                                                                                                      BP
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Pred. No. 15;
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                                                                No. 22;
                                                                                                                                                                                                                                                                                                                  36.6;
No. 22;
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No. 14
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                                    polypeptide
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4.
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Length 905;
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                                                                         Length
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Query Match
Best Local S
RESULT 754
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Best Local S
RESULT 748
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RESULT 752
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RESULT 753
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SULT 747
                                                                                                                                                                               Query Match
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                                                                                                                   ADQ25850 standard; DNA; 4145 BP. Rat G-protein coupled receptor 88 W02004054617-A1.
                                                                                                                                                                                                                  Nucleotide sequence WO200146387-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA47947 standard; DN Rice gene conferring WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                 AAZ06824 standard; DNA; 1294 BP.
Streptomyces albidoflavus chitobiosidase DNA
W09942594-A1.
                                                                                               01-JUL-2004.
(KYOW ) KYOW
                                                                                                                                                                                                                              AAH74537 standard; DNA; 1294 BP.
Nucleotide sequence of a chitobiosidase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice DNA sequence WO2003000905-A2.
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WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA69391 standard; DNA; 1182 Rice gene, SEQ ID 2714.
                      Rat G protein-coupled WO200136634-Al.
                                               AAH41184 standard;
                                                                                                                                                                                                        28-JUN-2001
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ry Match 2.5%; 9
Local Similarity 50.9%; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                    KYOWA HAKKO KOGYO KK.
h 2.5%;
Similarity 51.5%;
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KATAGIRI F.
KREPS J.
PROVART N.
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ZHU T.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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th 2.5%; Score
Similarity 49.7%; Pred.
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                                                                                                                                                                                            CORNELL RES FOUND INC.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DNA; 1182 BP.
Seq ID231 related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 1182
ng disease
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                                  DNA; 4164 BP.
led receptor,
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49.7%;
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Pred.
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Pred. No. 29;
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resistance
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                                                                     Score 36.6;
Pred. No. 53;
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Pred.
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                                  Strg,
                                                                                                                               coding sequence
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No. 28;
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No. 28;
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No.
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No
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29;
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28;
                                  coding sequence
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Best Loca
RESULT 761
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RESULT 755
SBBB
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RESULT 759
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                                                                                                                                          Query Match
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Best Local
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        ADA69502 standard; DNA; 450 Rice gene, SEQ ID 2825. WO2003000898-A1.
                                                                                        DNA clone originating WO2003057877-A1.
                                                                                                ACL19207 standard; DNA; 418 BP. DNA clone originating in barley
                                                                                                                                                                               ACL19211 standard; DNA; 409 BP.
DNA clone originating in barley containing
                                                                                                                                                                                                                                                      Maize gene confe
WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                                     Human secreted protein encoding sequence W02004035732-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     Corn seedling-derived polynucleotide US2003237110-A9.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS70697 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN44528 standard; DNA; 49806 BP Mouse genomic sequence mCG20647. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE59563 standard; DNA;
Human gene XM_038377, SI
WO2003016475-A2.
                                                                                                                                                                         WO2003057877-A1.
                                                                                                                                                                                                              (SYGN) SYNGENTA PARTICIPATIONS AGREE AND MATCH 2.5%; Score Local Similarity 52.7%; Pred.
                                                                                                                                                                                                                                                                            ADA49220 standard;
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                                                                                                                                                (UYNI-) UNIV JAPAN OKAYAMA.
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(FARB ) BAYER AG
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(FARB ) BAYER AG.
                                                                    UYNI-) UNIV JAPAN OKAYAMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2-SEP-2003
(SAGR-) SAG
                                                                                                                                                                                                                                                                                                                 FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                               Local Similarity
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48.1%;
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57.4%;
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46.7%;
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2.5%;
58.1%;
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57.0%;
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disease re
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SEQ ID
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SEQ ID
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No. 19;
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No. 62;
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No. 19;
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No. 19;
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No. 1.
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62;
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                                                                                                                                          409;
                                                                                                 sequence
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Query Match
Best Local S
RESULT 769
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Best Local Similarity
RESULT 764
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                             Banana gene conferring d
WO2003000906-A2.
                                                                                                        DNA clone originating in barley W02003057877-A1.
                                                                                                                                                                                    ADA69813 standard; DNA;
Rice gene, SEQ ID 3136.
WO2003000898-A1.
                                                                                           17-JUL-2003.
(UYNI-) UNIV JAPAN
                                                                                                                                                                                                                                                                                                ACH22587 standard;
Human adult ovary ous US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE 2.5%; Sry Match 2.5%; St Local Similarity 55.6%; F
                                                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                           ABV59448 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice gene confer
WO2003000906-A2.
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                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS
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   Local Similarity
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LABAT I.
STACHE-CRAIN I
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PROVART N.
RICKE D.
ZHU T.
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th 2.5%; Score
Similarity 48.1%; Pred.
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GOFF S A.
KATAGIRI F.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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  PARTICIPATIONS AG. 2.5%; Score ty 48.1%; Pred.
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, cDNA #967.
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2.5%;
46.7%;
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Pred.
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Pred. No. 21;
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No. 2
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   36.
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No. 2
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No. 20;
3.4;
23;
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21;
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Best Loc.
RESULT 777
ID ADC7'
DE P'
PN
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Best I
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Plant cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA homologous to WO2003020905-A2.
   ADC77183 standard;
DNA homologous to F
WO2003020905-A2.
                                                                             DNA homologous to phytopathogen resistance-related
                                                                                                                                       DNA homologous to WO2003020905-A2.
                                                                                                                                                        ADC75915 standard;
                                                                                                                                                                                                                                                                                                                                                                       Plant DNA sequence which confers altered metabolic characteristic #6471.
WC2003020936-A1.
                                                                                      ADC76482 standard; DNA; 784 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC76477 standard;
                                                                      WO2003020905-A2.
                                                                                                                                                                                                                                                                                              Plant cDNA #3638.
US2004016025-A1.
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                                                                                                                                                                                                                                                                                                              MDJ42638 standard;
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                                                                                                                                                                                                                                                                                                                                                                                       DK59088 standard;
                                                     (DOWC ) DOW CHEM
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                                    Local Similarity
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MOUGHAMER T.

BRIGGS S P.

COOPER B.

GLAZEBROOK J.
                                                                                                                                                                                         RICKE D.
ZHU T.
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ZHU T.
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KATAGIRI F.
KREPS J.
PROVART N.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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PROVART N.
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KATAGIRI F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
NA #3628.
           to phytopathogen
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                                                                                                                                               ; DNA; 716 BP.
phytopathogen
                    DNA; 784 BP.
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           resistance-related
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No. 24;
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No. 24;
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No. 23;
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No. 24
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No. 26;
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Best Loca
RESULT:783
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RESULT 780
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RESULT 779
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13-MAR-2003.
(DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
(DOWC ) DOW AGROSCIENCES LLC.
2.5%; S
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                            Lung cancer related WO200194629-A2. 13-DEC-2001.
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                                                                                                              Lung cancer related WO200194629-A2.
                                                                                                                                                                                            ABL67798 standard;
Oesophagus cancer:
WO200194629-A2.
                                                                                                                                                                                                                                                              DNA encoding novel WO200175067-A2. 11-OCT-2001.
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13-MAR-2003.
                                                                                                                         ABL65422 standard; DNA; 1306
Lung cancer related gene sequ
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Plant cDNA #3632.
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                                                         ABL66524 standard; DNA; 1306
                                                                                             (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                     (AVAL-)
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MOUGHAMER T.
BRIGGS S.
COOPER B.
GLAZEBROOK J.
GOFF S.
KATAGIRI F.
KATAGIRI F.
KATAGIRI P.
KATAGIRI J.
RICKE D.
RICKE D.
RICKE D.
ZHU T.
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                   AVALON PHARM.
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48.1%;
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48.1%;
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48.1%;
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ch confers
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  36.4;
No. 3
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No. 27;
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No. 26;
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No. 26;
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Best Local Similarity RESULT 787
 Query
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                                                                                                                                                                                                                                                                                                                                                                               Novel human nucl
WO2003102159-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE47781 standard; DNA; 1710 BP. Human NOV45b gene SEQ ID NO:143. W02003076642-A2.
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WO2004028479-A2.
08-APR-2004.
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 Match
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      TAUPIER R
CATTERTON
SHENOY S G
                                 ROTHENBERG I
SPADERNA S I
HJALT T.
                                                                   AGEE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
                                                                                                                                                                                                                                                                  ) ZERHUSEN B D.
PATTURAJAN M.
KEKUDA R.
) MILLER C E.
) RIEGER D K.
) PENA C E A.
) SHIMKETS R A.
                                                                                                                                       ANDERSON D W.
SPYTEK K A.
GERLACH V.
BURGESS C E.
KHRAMTSOV N V.
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CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
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VERNET C A M.
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sequence #4
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36.4;
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No. 38;
DВ
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1710;
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Best Local Similarity
RESULT 789
ID ABL67803 standard; D
DE Oesophagus cancer re
PN WO200194629-A2.
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RESULT 793
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RESULT 790
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                                         ACN44608 standard;
Mouse genomic seque
WO2003073826-A2.
                                                                                                     09-AUG-2001.
(HUMA-) HUMAN
                                                                                                                          AAK79963 standard; DNA; 5714
Human immune/haematopoietic
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                   AAS35076 standard; DNA; 32121 BP.
DNA #26 encoding human neoplastic
W0200155163-A1.
02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence #337 encoding no w0200155301-A2.
                                                                                                                                                                                                           ACN44094 standard; DNA; 35236 BP Human genomic sequence hCG23314. WO2003073826-A2.
                                                                                                                                                                                                                                                                                              Human neoplastic US2003082758-A1.
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ry Match 2.5%;
t Local Similarity 50.6%;
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                               2-SEP-2003
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xy Match 2.5%;
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h 2.5%;
Similarity 54.7%;
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                                                  lard; DNA; 90043 BP
sequence mCG22175.
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No. 1.
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No. 1.
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No. 2.8e+02;
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.7e+02;
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.7e+02;
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RESULT 805
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AAD16230 standard; DNA; 107820 sr.
AAD16230 standard; DNA; 107820 sr.
Human ATP-binding cassette transporter ABCC6
2.5%; Score 36.4; DB
ery Match
2.5%; Pred. No. 3e+02;
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ADB20869 standard;
MRP1 based cancer:
WO2003013533-A2.
                                                                                     ACF62750 standard; DNA; 186591 BP. Cancer based on CYP3A5 related polynucleotide SEQ WO2003013534-A2.
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Human MDR1 related
WO2003013535-A2.
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Human MDR1 related
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Human UGT1A1 gene :
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ry Match 2.5%;
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
2:Ty Match 2.5%; Score 3
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Human MDR1 related
WO2003013537-A2.
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2.5%; Score 36.4;
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Human UGT1A1 gene
WO2003013536-A2.
                   ADB87939 standard;
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ry Match 2.5%; Score 36.
t Local Similarity 53.5%; Pred. No.
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.9e+02;
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.9e+02;
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.9e+02;
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.9e+02;
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.2e+02;
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.2e+02;
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.2e+02;
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.2e+02;
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2e+02;
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Best Local Similarity RESULT 817
                             RESULT 825
                                                                                                          Best Local Similarity
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                                      Query Match
Best Local :
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                                                                                                                                                         ABS73398 standard;
DNA encoding human
WO200268600-A2.
                                                                                                                                                                                                                                                                                                                               Maize sucrose synthase EST #130.
US2003135870-A1.
AAD07361 standard;
Human DNA encoding
WO200136674-A2.
                                                                           Human myosin light WO9936531-A1.
                                                                                                 AAX87371 standard;
                                                                                                                                   06-SEP-2002.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                07-SEP-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                     Human polynucleotide WO200164835-A2.
                                                                                                                                                                                                                                                                                               (CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADB92118 standard;
Human MDR1 related
WO2003013535-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB92113 standard;
Human MDR1 related
WO2003013535-A2.
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Human MDR1 related
WO2003013537-A2.
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                                                       22-JUL-1999.
(ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                          AAI82080 standard;
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2.5%; Score 36.4;
Local Similarity 53.5%; Pred. No. 4.
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                                      Local Similarity
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de SEQ ID N
                                                                                                                                                                   DNA;
         DNA; 11 myosin
                                                                                      cDNA; 1120
chain cDNA.
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DNA sequence SEQ
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DNA sequence SEQ
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DNA sequence SEQ ID
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53.5%;
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                  1120
                                                                                                                                                                   1086 BP.
HF1948 mutant
         120 BP.
light
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NO 2140.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 4.
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Pred.
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core 36.4;
and. No. 4
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         chain
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No. 22
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No. 4.
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No. 4.
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4.2e+02;
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.2e+02;
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.2e+02;
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.2e+02;
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.2e+02;
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Quer
Best Lc.
RESULT 833
ID ABD16
DB Pse
PN U'
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Best Local Similarity
RESULT 832
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Best Local Similarity
RESULT 831
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RESULT 828
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RESULT 827
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Best Local Similarity
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(ASTR ) ASTRI
(ASTR ) ASTRI
                                                                                                     ADL62786 standard; DNA; 1941 BP.
Human ovarian cancer DNA marker #20998
                                                                                                                                                                                                                                                                                                                                                                                      ADM33386 standard; cDNA; Human PRO71267 encoding woc2004028447-A2.
                                                                                                                                                                        WO2004048938-A2.
                                                                                                                                                                                                                                                                                                          ADP13398 standard; DNA; 1120 BP. Renal cell carcinoma differentially W0200448933-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL69454 standard; DNA; Prostate cancer related WO200194629-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL62349 standard; DNA; 1120 Colon adenocarcinoma related
                US6551795-B1.
                           Pseudomonas
                                                                                             WO200170979-A2.
                                                                                                                                                                                           ADQ22648 standard;
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WO2004028479-A2.
08-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colon adenocarcinoma WO200194629-A2.
                                    ABD16767 standard;
                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS
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                                                      Local Similarity
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                                                      MILLENNIUM PREDICTIVE MEDICINE th 2.4%; Score 36.2. Similarity 46.9%; Pred. No.
                                                                                                                                                                                                                              DORNER A.
STOVER J A.
SLONI D K.
                                                                                                                                                                                                                                                                     WYETH.
TWINE N C.
BURCZYNSKI
GENOME THERAPEUTICS CORP
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                         andard; DNA; 1989 BP.
aeruginosa polynucleotide
                                                                                                                                                                                 ; DNA; 1303 BP.
sarcoma-upregulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
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sequence #45.
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48.8%;
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UK LTD.
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45.9%;
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Pred. No. 35;
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Pred. No. 47;
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No. 35;
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No. 35;
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RESULT 842

ID AAQ55145 standard; I
DE Pseudomonas acruginc
PN W09401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM I
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ID AAD494
DE Human
PN WO2002
PD 31-OCT
PA (INCY-
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ID AAA384
DE Human
PN EP9992
PD 10-MAY
PA (UYPA-
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Best Local Similarity
RESULT 836
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                                                                                                                                                                                                                                                             Human intracellular signalling protein coding WC2002101008-A2.
                                                                                                                                                                                                                                                                                                                                                 AAA38444 standard; DNA; 2893 BP.
Human desmin gene 5' flanking re
EP999278-A1.
                                                                                                             ADL13006 standard; cDNA; 5467 BP.
Human steroid-induced C3A liver cell
                                                                                                                                                                                 Human vesicle-associated WO200286061-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACA51409 standard; DNA; 2355 BP. Prokaryotic essential gene #33066 WO200277183-A2.
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                              Pseudomonas aeruginosa
                                                                                                   US6673549-B1.
                                                                                                                                                                                                        AAD49464 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ABD16799 standard; DNA;
Pseudomonas aeruginosa p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA52522 standard;
                                                                       ry Match
                                                                                                                                         (INCY-) INCYTE GENOMICS INC.

CY Match 2.4%;

Local Similarity 50.3%;
                                                                                                                                                                                                                                                                                                        (UYPA-) UNIV PARIS VII.
2.4%;
CY Match 2.4%;
Local Similarity 52.3%;
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ry Match 2.4%; 
Local Similarity 48.3%;
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(REAS-) RES ASSOC
                                                                                                                                                                                                                                             INCY-) INCYTE GENOMICS INC.
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                                         DNA; 9515
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55.0%;
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50.3%;
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                                                                                                                                                                                           5230 BP.
protein-8
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EQ ID
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; Score 36.2; [
; Pred. No. 54;
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                               BP.
P2-2
                                                                                                                                          Score
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No. 60;
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No. 57;
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No. 51;
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No. 47;
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No. 48
                                                             36.
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76;
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78;
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                                                                                                                                                                                                                                                                                                                                                           promoter region
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Query Match
Best Local S
RESULT 850
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                                                      Best Local Similarity RESULT 851
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Best Local Similarity
RESULT:843
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Best Local :
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                                                                                                                                                                                                                                           AAZ87283 standard; DNA; 15872 BP. S. venezuelae vep ORF 1, SEQ ID N WO200000620-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa microbe identification-related WO200299133-A1.
                  Mouse genomic se
WO2003073826-A2.
                                                                                                                                                ADL91929 standard; DNA; 15872
Streptomyces venezuelae vep OF
US2003194784-A1.
                                                                                                                                                                                                                                                                                                                                                      AAT68715 standard; DNA; 15872 BP.
Streptomyces venezuelae polyketide synthase vep
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine DGAT gene WO2003004630-A2.
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:ry Match 2.4%; Score 36.2; DB 10;
t Local Similarity 50.9%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ77045 standard;
Bovine DGAT gene SI
WO2003004630-A2.
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                                           ACN44556 standard;
                                                                                                   (SHER/) SHERMAN D
(LIUH/) LIU H.
(XUEY/) XUE Y.
                                                                                                                                                                                                                       (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                     06-JAN-2000
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                                                                                                                                                                                                                                                                                                                                            WO9722711-A1.
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                                                                                           (ZHAO/)
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th 2.4%;
Similarity 44.5%;
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h
2.4%; Score 36.2; DB 10;
Similarity 50.9%; Pred. No. 1.2e+02;
                                                                                         ZHAO L.
                             dard; DNA;
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SEQ ID NO:1.
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SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                           2.4%;
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designated PS-2.
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44.5%;
                                 mCG21411.
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Pred.
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                                                                                                                                                            coding sequence
                                                                   36.
No.
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                                                                   DB 12;
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.3e+02;
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.1e+02;
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SAGRES DISCOVERY

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                                                                                                            RESULT 860
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RESULT 855
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RESULT 854
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Best Local Similarity
RESULT 852
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Best Local Similarity
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                                                                            ABD32868 standard; DNA; Human cancer-associated WO2004074320-A2.
ADQ19085 standard;
Human soft tissue s
WO2004048938-A2.
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EP806480-A2.
                                      (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.4%;
t Local Similarity 48.3%;
                                                                                                                                    (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                           MO2004060304-A2.
                                                                                                                                                                    ADQ97107 standard; DNA; Mouse cancer associated
                                                                                                                                                                                                                                                                     Murine cancer-associated WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                            WO2004067740-A1.
12-AUG-2004.
(EFAR-) EFARMES SA.
                                                                                                                                                                                                                                                                                                                                                           ADR28249 standard; DNA; 59999 Human low density lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT80413 standard;
Tylactone synthase
EP791655-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer-associated WO2004058146-A2.
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Streptomyces roseofulvus frenolicin gene cluster
                                                                                                                                                                                                                                                                                       ABD33301 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABD33195 standard; DNA;
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ry Match
2.4%; Score 36.2; DB 2;
t Local Similarity 55.0%; Pred. No. 1.6e+02;
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                                                                                                                     Local Similarity
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           sarcoma-upregulated
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                     DNA; 452 BP.
                                                                                                                                                                                                                                                                                        DNA;
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2.4%; Score:
55.0%; Pred. 1
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51.7%;
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56.2%;
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d (CA)
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                                                                                       238417 BP.
genomic DNA HD17-053.
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sequence MD08-002,
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gene cluster.
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gene
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e 36.
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No. 3.
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No. 3.1e+0
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No. 3.
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No. 1
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                                      5.2; DB
5.5e+02;
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.6e+02;
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.5e+02;
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.1e+02;
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..7e+02;
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.6e+02;
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.2e+02;
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.6e+02;
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.6e+02;
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Query Match
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RESULT 862
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RESULT 868
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RESULT 865
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                                                      Prokaryotic essential gene #23755. WO200277183-A2. 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                 ABD02947 standard; DNA; 1512 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banana gene conferring disease resistance W02003000906-A2.
                                                                                                                                                                                                                                                                    ABD03012 standard; DNA; 1677 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS PART 2.4%;
IT Match 2.4%;
It Local Similarity 49.2%;
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:ry Match 2.4%; Score

:r Local Similarity 46.7%; Pred.
                                                                                                                                                                                      Bacterial polynucleotide US2003233675-A1.
                                                                                                                                                                                                          ADT44558 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays DNA fragment SEQ ID EP1033405-A2.
         AAF16277 standard; cDNA; 3779
                                                                                                                                       (HINK/) HINKLE G
(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa polynucleotide #10016
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABD11412 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC40977 standard; DNA; 507
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Zea mays DNA fragment SEQ ID
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prostate cancer antigen
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                                               ELITRA PHARM INC
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                                                                                                                                                                                                                                                                                                           2.4%;
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                            2.4%;
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46.7%;
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e #19309.
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ID NO: 30530.
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NO:712
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WO200055174-A1.

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RESULT 878

ID ADH62916 standard, DNA, 2
DE Human Jagged 2 gene.
PN US2003170636-A1.
PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
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(UNIW ) UNIV WASHINGTON.
(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
2.4%; Score 36;
                                                                                                 ADD00956 standard; DNA;
Human Jagged 2 encoding
                                                                                                                                                               ABQ99655 standard; DNA; Human membrane spanning WO200262946-A2.
                                                                                         Human Jagged 2 e
WO2003077848-A2.
                                                                                                                                                                                                                                        Human musculoskeletal system-associated US2004009488-A1.
                                                                                                                                                                                                                                                            ADJ30229 standard;
                                                                                                                                                                                                                                                                                              (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                   cDNA encoding novel US2002147140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Human musculoskeletal system WO200155367-A1.
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Human musculoskeletal system related polynucleotide
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WO9858958-A2
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(ROSE/) ROSEN C
                                                                                25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                      ABX59479 standard;
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cy Match
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1.5e+02;
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2e+02;
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN F
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(INCY-) INCYTE GENOMICS INC.
2.4%;
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Human genomic sequence l
WO2003073826-A2.
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US2003207839-A1.
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Human foetal brain cDNA #5160.
US2003073623-A1.
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Mouse genomic sequence mCG2215.
WO2003073826-A2.
                                                                                                                                                               ADJ11721 standard; DNA; 561 BP.
Rice cDNA modulated by post-transcriptional gene
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WO2003073826-A2.
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(LABA/) LABAT I.
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COOPER B.
GLAZEBROOK J.
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KATAGIRI F.
KREPS J.
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th 2.4%;
                   RICKE D.
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                             MOUGHAMER T. PROVART N.
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Rice gene, SEQ ID 3822.
WC2003000898-A1.
                                                                          Sequence encoding F-box WO200012679-A1.
                         cDNA of Human F-box
                                                                                                                                                          ABT42404 standard;
Toxicity modelling
                                                                                                                                                                                                                  ADB53815 standard; DNA; 648 BP. Primary rat hepatocyte toxicity modelling W02003065993-A2.
                                                                                                                                                                                                                                                                                      Toxicity-related gene, WO2003064624-A2.
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(ZHUT/) ZHU T.
(WANG/) WANG X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice gene conferring disease WO2003000906-A2.
                WO200255665-A2.
                                                                                                                                                                                                                                                                                             ADB59062 standard; DNA; 648
Toxicity-related gene, SEQ
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Rice DNA modulated
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                                AAL41056 standard;
                                                (UYNY) UNIV NEW YORK STATE.
ry Match 2.4%;
t Local Similarity 51.7%;
                                                                                                                                                                                                  (GENE-) GENE LOGIC INC.
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(GENE-) GENE LOGIC
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COOPER B.
GLAZEBROOK J.
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PROVART N.
RICKE D.
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h 2.4%; Score
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US6551795-B1.
                                                                                                                                                                                                                                                                                               Human protein en WO2004009834-A2.
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EP1347046-A1.
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Novel human cDNA SEQ ID NO 408.
US2003104529-A1.
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ADH76501 standard; DNA; 2572 BP.
727 amino acid human neurotransmitter transporter protein
                                                                                                                      29-JAN-2004.
                                                                                                                                    Human protein encoding WO2004009834-A2.
                                                                                                                                                                             ADM86960 standard;
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ry Match 2.4%; Scc
t Local Similarity 56.3%; Pre
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(TANG/) TANG Y T.
                                                                                               (NUVE-) NUVELO INC
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encoding cDNA SEQ ID
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GPCR-like ]
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US2003219774-A1.

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Human therapeutic WO2004080148-A2.
                                                                                                                                                                                                                                          AAS72201 standard; cDNA; DNA encoding novel human WO200175067-A2.
                                                  wozoo4065545-A2.
                                                                                                                ACN40359 standard; cDNA; 361
Tumour-associated antigenic
WO2004030615-A2.
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Rice DNA modulated
US2003135888-A1.
                                                                    ADR25659 standard; DNA;
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(LEEL/) LEE L M.
                              ROSE-) ROSETTA INPHARMATICS LLC. NECA-) NETHERLANDS CANCER INST.
AD36022 standard;
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GOFF S A.
KATAGIRI F.
KREPS J.
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WANG X.
CHANG H.
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WESTPHAL R.
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COOPER B.
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Best Local Similarity RESULT 910
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                                                                                     ABZ32962 standard; cDNA; 174 E
Human colon tumour cDNA clone
WO200283070-A2.
24-OCT-2002.
                Corn seedling-de
US2003237110-A9.
25-DEC-2003.
                                                                                                                                                                     ABZ33005 standard; cDNA; 174 I
Human colon tumour cDNA clone
WO200283070-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human WO200037643-A2.
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Mouse cancer associated sequence MD10-020,
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Colon tumour related determined
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                                           ADS67683 standard;
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ry Match 2.4%;
t Local Similarity 57.1%;
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PHARM INC.
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Probe #13248 for ger
WO200157278-A2.
09-AUG-2001.
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(MOLE-) MOLECULAR DYNAMICS INC.
2.4%; Score
2.7%; Pred.
                                 Probe #17322 used to
                                        AAI48636 standard;
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Human foetal liver
WO200157277-A2.
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DNA encoding novel
WO200175067-A2.
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Cotton androecium t
US2004123340-A1.
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17-JUL-2003.
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(FISH/) FISHER D
(LIUJ/) LIU J.
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(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
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(MOLE-) MOLECULAR DYNAMICS I
(MOLE-) MOLECULAR DYNAMICS I
2.4%;
ery Match 2.4%;
45.9%;
                                                                                                                                                                     Human genome-derived single WO200186003-A2.
                                      WO200218632-A2.
                                                                                               Oligonucleotide WO200218632-A2. 07-MAR-2002.
                                                                                                               ABQ19226 standard; DNA; 687 BP
Oligonucleotide for detecting
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Human liver single
WO200157273-A2.
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Human breast cell
WO200157271-A2.
                                                       ABQ19227 standard;
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Probe #13879 for go
WO200157274-A2.
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ry Match 2.4%;
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41;
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                                              methylation
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RESULT 943
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO W0200153312-A1.
                                                                                                                                                           ABA55830 standard;
Human foetal liver
WO200157277-A2.
                                                                                                                                                                                                                                                                                                           Human cDNA sequence EP1074617-A2.
                        Human breast
                                                                                              Probe #4172 used to
                                                                                                         AAI35486 standard;
                                                                                                                                                                                                                                    Probe #4038 for WO200157278-A2.
                                                                                                                                                                                                                                                      AAI14105 standard; DNA; 1969
                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
ry Match 2.4%;
t Local Similarity 47.0%;
                                                                                                                                                                                                                                                                                                                   AAH15073 standard; cDNA; 1790 BP.
Human cDNA sequence SEQ ID NO:13081.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC35370 standard; DNA; 760 BP.
                                                 (MOLE-) MOLECULAR DYNAMICS INC.
ry Match 2.4%; Sc.
Local Similarity 45.9%; Pr
                                 ABA45341 standard;
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) HINKLE G J.
) SLATER S C.
) CHEN X.
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                        cell single
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single exo
                                                                                                        DNA; 1969 BP.
                                                                                              measure
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52.0%;
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No. 43;
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No. 69;
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No. 43
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42;
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Best Local Similarity RESULT 951
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RESULT 948
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                                                                                                                                       Human cell cycle and prolifera W0200107471-A2.
01-FEB-2001.
(INCY-) INCYTE GENOMICS INC.
puery Match 2.4%; Suest Local Similarity 47.0%; P
                                                                                                                                                                                                                                             Human genome-derived single exon W0200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
214 Score 2.4%; Score
Et Local Similarity 45.9%; Pred.
                                                                                                  ADE47789 standard;
Human NOV45f gene (
WO2003076642-A2.
                                    ADH41892 standard; DNA; 2
Novel human nucleic acid
                                                                                                                                                                                     AAF59600 standard; cDNA; 2035 BP. Human cell cycle and proliferation
                                                                                                                                                                                                                                                                                                                                        AAI03958 standard; DNA; 1969 BP.
Probe #3949 used to measure gene
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2.4%; Sc
t Local Similarity 45.9%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK04048 standard; DNA; 1969
Human brain expressed single
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                            Novel human nucleic
WO2003102159-A2.
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                                                               Local Similarity
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h 2.4%;
Similarity 45.9%;
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         CORP.
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expressed single
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45.9%;
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57.0%;
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2.4%;
                                    2066 BP.
d NOV36a.
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D NO:151.
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Pred.
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No. 70;
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No. 69;
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Length 2066;
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Best Local Similarity
RESULT 956
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                                                                                     Query Match
Bacterial polynucleotide US2003233675-A1.
                                                   AAC48435 standard; DNA; 2173 BP. Arabidopsis thallana DNA fragment EP1033405-A2.
                                                                                                       Human macrophage
KR2003003840-A.
                                                                                                                  ADO54827 standard;
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Human NOVX protein
US2004014053-A1.
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                                  Local Similarity
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CATTERTON E.
SHENOY S G.
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DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
                                                                                          PANGENOMICS
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SPADERNA S
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RASTELLI L.
AGEE M L.
CHAUDHURI A.
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VERNET C A M.
LEITE M W.
GUO X S.
ANDERSON D W.
SPYTEK K A.
CEBTACK V
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ZHONG M.
CASMAN S J.
VOSS E Z.
BOLLDOG F L.
PADIGARU M.
SMITHSON G.
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BURGESS C E.
KHRAMTSOV N V.
                                                                                                                                                                                                                                                                                                                                                                                     ZERHUSEN B
PATTURAJAN
KEKUDA R.
MILLER C E.
RIEGER D K.
PENA C E A.
SHIMKETS R
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                                                                                                           1; DNA; 2136 stimulating
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2.4%;
57.0%;
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57.0%;
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              2205 BP. #20582.
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Pred.
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                                No. 72;
                                                                                                                               35.6; I
No. 71;
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No. 72;
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RESULT 964
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RESULT 958
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                                                                AAT62437 standard;
Human L5/3 partial
US5606029-A.
25-FEB-1997.
                                                                                                                                                                                                                                                AAQ79723 standard; cDNA to mRNA; 2219 BP. Human L5/3 tumour suppressor gene (Cy8214 US5315000-A.
                                                                                                                                                               AAT62436 standard;
Human L5/3 partial
US5606029-A.
                                                                                                                                                                                                                                                                                                                                       AAQ79724 standard; cDNA to mRNA; 2219 BP. Human L5/3 tumour suppressor gene (Phe214 US5315000-A.
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(SLAT/)
(CHEN/)
(GOLD/)
                                                     (CHIL-) CHILDREN'S
                                                                                                                                                      25-FEB-1997
                                                                                                                                                                                                       (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
ry Match
2.4%; Score 35.6;
t Local Similarity 57.0%; Pred. No. 73
                                                                                                                                                                                                                                                                                                                                                                                                                             Human hepatocyte WC200283074-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macrophage s
EP750040-A2.
                                                                                                                                                                                                                                                                                                                                24-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV75112 standard;
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(BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MSP cDNA.
                                                                                                                                                                                                                                                                                                                   (CHIL-) CHILDRENS HOSPITAL MEDICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV72083 standard;
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Macrophage stimulating protein C672 deletion
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                                 Local Similarity
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CHEN X.
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d; cDNA; 2219 BP.
related nucleotide sequence
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                                                  HOSPITAL MEDICAL CENT.
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2.4%; Score 35.6;
57.0%; Pred. No. 73;
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2.4%;
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                                                                                                                                                                         cDNA to mRNA; 2219 BP. clone #33 polymorphism
                                                                                    cDNA to mRNA; 2219 BP. clone #33 polymorphism
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2.4%;
57.0%;
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factor-like
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; Score 35.6; I
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Score 35.6; I
Pred. No. 73;
                               Score 35.6;
Pred. No. 73;
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Best Local
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(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
                                                                                               ACN41133 standard; cDNA; 2493 BP.
                                                                                                                                                        Human polynucleotide SEQ WO200153312-A1.
                                                                                          Human diagnostic WO2004023973-A2.
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                   WO2003018612-A2.
                            ACC42370 standard; DNA; 2573
Human extracellular messenge:
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06-MAR-2003.
                                                                                                                                                                                                                                               Human extracellular messenger,
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Human tumour-associated;
WO2004060270-A2
                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.

CY Match 2.4%;
Local Similarity 57.0%;
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Leukaemia-related DNA sequence
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ry Match 2.4%;
t Local Similarity 57.0%;
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ry Match 2.4%; Score
Local Similarity 57.0%; Pred.
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(SCHO/) SCHOCH C.
(KERN/) KERN W.
                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM (UYLU-) UNIV LUDWIG MAXIMILIANS.
                                                                        INCY-) INCYTE
                                                                                                                                              HYSE-) HYSEQ INC.
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971
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   INCYTE GENOMICS INC
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57.0%;
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47.0%;
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2 ID NO 1719.
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; Pred. No. 74;
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No.
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No. 74;
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No. 73;
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78;
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RESULT 976
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07-FEB-2001.
(HELI-) HELIX RES INST.
(HELI-) 2.4%; (
Match 2-vity 47.0%;
                                                        Human tumour suppressor mRNA (6997 W02003058201 A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human extracellular messenger WO2003002610-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial polynucleotide US2003233675-A1.
                (QUAR.) QUARK BIOTECH INC.
(CLEV-) CLEVELAND CLINIC FOUR
EXY Match 2.4%;
It Local Similarity 51.2%;
                                                                                                                                                                                                                                                                                                                                                                                      AAH17866 standard; cDNA;
Human cDNA sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN41131 standard; cDNA; 2589 BP. Human diagnostic and therapeutic WO2004023973-A2. 25-MAR-2004.
                                                                                                                                   WO200175067-A2.
11-OCT-2001.
                                                                                                                                                     DNA encoding novel
                                                                                                                                                                                                                      Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.

RY Match 2.4%;

t Local Similarity 57.0%;
                                                                                                                                                                                                                                                                                                 Human extracellular messenger,
WO2003018612-A2.
 AAQ25975
                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                              AAS65913 standard;
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ry Match 2.4%;
t Local Similarity 57.0%;
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standard; DNA; 15377 BP.
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human diagnostic
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Pred. No. 1.3e+02;
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82;
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RESULT 988
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Best Local Similarity
RESULT 987
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                                   WO2004060304-A2.
                                          ADQ97526 standard; DNA; 151052 BP.
Mouse cancer associated sequence MD09-009,
                                                                                                              02-SEP-2004
                                                                                                                        WO2004074320-A2.
                                                                                                                                ABD32827 standard; DNA; 129381 BP. Human cancer-associated genomic DN
                                                                                                                                                               (SAGR-) SAGRES DISCOVERY.

ry Match
2.4%;
t Local Similarity 54.6%;
                                                                                                                                                                                                            ACN44586 standard; DNA; 118931 BP. Human genomic sequence hCG30014. W02003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                          ABD33589 standard; DNA; 92219 Murine cancer-associated (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer associated WO2004060304-A2. 22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcp gene cluster.
                                                                                                                                                                                                                                                                                                                                                                   WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ59365 standard; DNA; Human cancer-associated WO2004058288-A1.
                                                                                                                                                                                                    L2-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABD32540 standard; DNA;
Human cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                          (SAGR-) SAGRES DISCOVERY INC.
cy Match 2.4%;
Local Similarity 57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ97278 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS73531 standard;
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ry Match 2.4%;
t Local Similarity 46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD32540 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MH mutant porcine ryanodine receptor cDNA WO9211387-A1.
                                                                                                                                                                                                                                                                                                                                           SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UTOR ) UNIV TORONTO (UYGU-) UNIV GUELPH.
                                                                            ocal Similarity
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                                                                                                 SAGRES DISCOVERY INC.
              SAGRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGRES DISCOVERY INC. h 2.4%; Similarity 53.6%;
  DISCOVERY INC.
2.4%;
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                                                                           2.4%;
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57.0%;
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sequence HD08-025,
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genomic DNA
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gene
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Pred. No. 1.
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No.
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No. 5.
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  35.6;
                                                                                                                                                              35.6; DB 11;
No. 5.3e+02;
                                                                                                                                                                                                                                                      35.6;
No. 5.
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No. 4
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No. 3.
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No. 4.7e+02;
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4.
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                                                                           DB 13;
.5e+02;
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1.5e+02;
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.1e+02;
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.4e+02;
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.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
.4e+02;
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.9e+02;
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  12;
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Length
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Query Match
Best Local Similarity
RESULT 1001
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RESULT 998
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Best Local Similarity
RESULT 999
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RESULT 996
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RESULT 994
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B napus caltractin-like WC2004070035-A2.
                                                                                                                                                                                   Pseudomonas aeruginosa polynucleotide US6551795-B1. 22-APR-2003.
                                                               (MATH/) MATHIALAGAN
(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                      US2002137139-A1.
26-SEP-2002.
                                                                                                                           ABX37512 standard; cDN
Bovine EST associated
                                                                                                                                                                                                                                                                                                   ABX36854 standard; cDNA; 41
Bovine EST associated with
US2002137139-A1.
26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABX42580 standard; cDNA; 41 Bovine EST associated with US2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel W0200175067-A2. 11-OCT-2001.
                                                                                              (BYAT/) BYATT J C
                                                                                                                                                                               (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS90684 standard;
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Bovine EST associated with
US2002137139-A1.
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(MATH/) MATHIALAGAN
(TAON/) TAO N.
                                                                                                                                                                                                                                                                                                                                                                      (WARR/) WARREN W C
                                                                                                                                                                                                                                                                                                                                                                                 (TAON/) TAO
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(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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(GENE-) GENE LOGIC
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                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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MATHIALAGAN
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ted with
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human diagnostic
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                                                                                                                                                         49.8%;
                                             2.4%;
47.2%;
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47.2%;
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               428 BP.
protein
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                                                                                                                         428 BP.
ch lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                    416 BP.
th lactation/muscle/fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201143 BP. expressed
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th lactation/muscle/fat deposition
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lactation/muscle/fat
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Pred.
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              coding
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No. 36;
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No. 36;
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.8e+02;
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               SEQ
                                                                                                                           deposition #2677.
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               NO:
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Query Matc
Best Local
RESULT 1008
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Qq
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA69809 standard; DNA;
Rice gene, SEQ ID 3132.
WO2003000898-A1.
ACF34491 standard; DNA; 1526
                                                                                               ADQ85345 standard; cDNA; 1525 BP.
Human tumour-associated antigenic target (TAT)
                                                                                                                                                                                               ADQ83950 standard; cDNA; Human tumour-associated a WO2004060270-A2.
                                                                                                                                                                                                                                         (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.

ry Match
2.4%; Score 35.4; DB
Local Similarity 49.2%; Pred. No. 56;
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02-OCT-2003.
                                                                                                                                                                                                                                                                                                 M lichenicola melithiazol synthesis
                                                                                                                                                                                                                                                                                                                                                                             Human BSK-36-8 complementary strand EP1310567-A2.
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Human adult brain cDNA #1737.
US2003073623-A1.
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                                                                                                                                                    (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                           ACF04830 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                 ADE76270 standard; DNA; 701 BP.
                                          (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN
(TAON/) TAO N.
                                                                                       102004060270-A2
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2.4%; Score 35.4;

Similarity 48.3%; Pred. No. 43
                                                                                                                                                                                                                                                                                                                                                       OLIGENE GMBH.
                    Similarity
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                    2.4%;
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2.4%;
48.7%;
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47.2%;
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No. 37;
                    35.4;
No. 69
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No. 69;
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No. 38;
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                                                                                               cDNA sequence #2159
                                                                                                                                                                                                           cDNA sequence #764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deposition
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Best Local Similarity
RESULT 1011
ID ADPRIANT
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Best Local Similarity
RESULT 1017
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RESULT 1014
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Best Local Similarity
RESULT 1010
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Best Local
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15-APR-2004.
(GETH ) GENENTECH INC.
2.4%;

MATCH 2.4%;
47.2%;
         Human dithp intr
WO200297031-A2.
05-DEC-2002.
(INCY-) INCYTE G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2003.

16-JAN-2003.

(MILL-) MILLENIUM PHARM INC.
2.4%;

ary Match
2:4%;
47.2%;
                                                                                                                                                                                                     ACN92807 standard; DNA; 3535 I
Breast cancer related marker,
US2003099974-A1.
29-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukaemia-related DNA sequence #1976. WO2003039443-A2.
                                                                                                                       ADI24476 standard; cDNA; 3718 Human modifier of Chk1 (MCHK) W02004004785-A1.
                                                                                                                                                                                                                                                                                                                                                                                      AAT91855 standard; cDNA; 1559
DUB-1 enhancer/promoter.
WO9706247-A2.
20-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC50093 standard; cDNA; Breast cancer associated WO2003004989-A2.
                                                        ACC46250 standard;
                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
ry Match 2.4%;
t Local Similarity 47.2%;
                                                                                                                                                                                                                                                                                                         Prokaryotic essential WO200277183-A2.
                                                                                                                                                                                                                                                                                                                    ACA39654 standard; DNA; 1770 BP.
Prokaryotic essential gene #21311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding angiogenesis protein
                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN39732 standard; cDNA; 1526 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
(UYLU-) UNIV LUDWIG MAXIMILIANS.
(HAFE/) HAFERLACH T.
                                                                                                   (EXEL-) EXELIXIS INC.
                                                                                                               L5-JAN-2004
                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
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SCHOCH C.
KERN W.
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th 2.4%; Score 3.
Similarity 51.6%; Pred. N
                                          ındard; cDNA; 3978
intracellular sigr
 GENOMICS
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52.3%;
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47.2%;
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CDNA
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signalling
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Pred. No. 70;
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No. 69;
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No. 69;
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No. 1.
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No. 74;
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                                           protein-encoding
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Length 3978;
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                                                                                                                                     NO:26
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Best Local
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RESULT 1024
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                                                                                                                                                                                 Query Match
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                                          ABD32684 standard; DNA; Human cancer-associated WO2004074320-A2.
                                                                                                                           ADQ97945 standard; DNA; 39414 BP. Mouse cancer associated sequence WO2004060304-A2.
                                                                                                                                                                   (ISIS-) ISIS PHARM INC.

ry Match
2.4%;
t Local Similarity 53.2%;
                                                                                                                                                                                                    WO200288162-A1.
                                                                                                                                                                                                                       AAD52172 standard; DNA; 26000 BP.
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                                                                                                                                                                                                                                   AAD52172 standard;
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                                                                                                                                                                                                                                                                                                            Human cancer-associated
                                                                                                                                                                                                                                                                                                                     ABD33393 standard;
                                                                                                       (SAGR-) SAGRES DISCOVERY INC.
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ry Match
Local Similarity 46.2%;
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RY Match
2.4%;
t Local Similarity 59.7%;
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                     SAGRES DISCOVERY INC.
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                                                                                  2.4%;
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antigen 2
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No. 3.
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No. 2.
35.4; DB 13;
No. 3.6e+02;
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No. 2.7e+02;
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No. 1.
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No. 1.3e+02;
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.8e+02;
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.2e+02;
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.2e+02;
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.2e+02;
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        Length 41991;
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Query Match
Best Local S
RESULT 1030
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Best Local Similarity
RESULT 1034
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ID ACF0481
DE Melithi
PN WO20030
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RESULT
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                                                     ADG70184 standard; DNA; 379652 DNA of BAC bA236m15-00303.
                                                                                                                                  ABX16390 standard; DNA; 6 Mouse high growth region. US2002155564-A1.
                                 03-JAN-2003
                                                                                                                                                                                                                         US2004072154-A1.
15-APR-2004.
                                                                                                               (REGC
                                                                                                                                                                                                   (ENGE/) ENGELHARD
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                                                                                                                                                                                                                                                                                                              30-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADA02807 standard; DNA; 96597 BP. Mouse Fish carcinoma associated c
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ry Match
t Local Similarity 51.6%;
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"YY Match 2.4%;
"It Local Similarity 47.5%;
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                                                                                                                                                                                                             MORR/) MORRIS D W
                                                                                                                                                                                                                                                                                                                                                                                         (SAGR-) SAGRES DISCOVERY.
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ry Match
2.4%; Score 35.4;
t Local Similarity 49.2%; Pred. No. 40
 Local Similarity
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                                                                                                          UNIV CALIFORNIA.
                      ISIS INNOVATIONS LTD.
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h 2.4%;
Similarity 51.6%;
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54.1%;
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Ciated (CA)
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35.4; DB 10;
No. 5.8e+02;
                                                                                     35.4;
No. 5.
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No. 5.
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No. 5.
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4e+02;
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.8e+02;
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.4e+02;
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.4e+02;
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.4e+02;
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.1e+02;
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          Length 110000;
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Best Local Similarity
RESULT 1043
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Best I
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22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
2.4%;
ery Match 2.4milarity 50.9%;
                              Thale cress cDNA repressed in WO2004035798-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABD32886 standard; DNA; Mouse cancer-associated WO2004074320-A2.
                                                                                                             Rice gene conferring WO2003000906-A2.
                                                                                                                   ADA48417 standard; DNA; 500 BP.
Rice gene conferring disease resistance
                                                                                                                                                                                                                                                                                          WO200228999-A2.
                                                                                                                                                                                                                                                                                                Human cDNA differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                    ADP80536 standard; DNA; 118788
Human HPC2/ELAC2 gene SeqID1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABD32911 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ97050 standard; DNA;
                                                                       (SYGN ) SYNGENTA PARTICIPATIONS AG

ry Match 2.4%; Score

Local Similarity 48.1%; Pred.
                                                                                                                                                                                                                US2002137139-A1.
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                                                                                                                                                                                                                                  ABX39880 standard;
                                                                                                                                                                                                                                                                                                           ABK83573 standard;
                                                                                                                                                                                    (BYAT/) BYATT J C.
MATH/) MATHIALAGAN
                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                                             TP2004166565-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY INC.
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Local Similarity
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A/) WATANABE M.
J/) FURUSATO M.
B ) YAKULT HONSHA |
                                                                                                                                                                  WARREN W C.
                                                                                                                                                                            TAO N.
                  CROPDESIGN
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63.5%;
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2.4%;
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2.4%;
46.2%;
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No. 46;
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No. 45;
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5.6e+02;
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6e+02;
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.8e+02;
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.8e+02;
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Query Match
Best Local S
RESULT 1048
                   Best Local
RESULT 1053
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Best Local Similarity
RESULT 1052
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RESULT 1051
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RESULT 1049
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                                     (TIGR-) TIGR INSI COULAGE MADEL (QUIA-) QUIAGEN GMBH.
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
(MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
(MEDI-) MEDIZINISCHE HOCHSCHULE HOCHS
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DE19935088-A1.
01-FEB-2001
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Arabidopsis thaliana
EP1033405-A2.
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                                                                                                                                                                                                                                                                                                                                    Human cDNA encoding WO200214358-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACL20017 standard; DNA; 708 BP. DNA clone originating in barley W02003057877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACL20023 standard; DNA; 6
DNA clone originating in
WO2003057877-A1.
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W02003020905-A2.
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   ADA02845
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Human cDNA encoding novel secreted
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. Similarity 53.7%;
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HINKLE G J.
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CDNA; 2403 BP.
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RESULT 1057
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                                                                                                                                                                                                          Mouse Fgfr3 carcinoma associated cDNA, WO2003057146-A2.
                                                         Mouse Fgfr3 genomic WO2003045230-A2.
                                                                                                                                   ADB72582 standard; mRNA; 2887 Mouse Fgfr3 mRNA. WO2003008583-A2.
                                                                                                                                                                                                                                                                       HOMO protein encoding WO2004014946-A1.
19-FEB-2004.
(NEWO-) NEWORGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                     AAZ09484 standard; DNA; 2606 Bovine retina Ih ion channel W09942574-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Murine carcinoma associated
US2004072154-All.
15-APR-2004.
(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC85323 standard;
                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Fgfr3 mRNA sequence. WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB72583 standard; cDNA;
Mouse Fgfr3 cDNA.
W02003008583-A2.
                                                                                                                                                                                                                                                                                                              ADK00684 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Fgfr3 carc WO2003057146-A2.
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                    Local Similarity
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th 2.4%;
Similarity 51.2%;
                  SAGRES DISCOVERY.

2.4%;
Similarity 51.2%;
  standard;
DNA; 2887
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c sequence.
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48.1%;
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Pred.
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DNA fragment.
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No. 1.
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No. 98;
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No. 98;
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98;
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.1e+02;
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.1e+02;
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Query Match
Best Local Similarity
RESULT 1068
Query Match
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RESULT 1069
                                                                                                                     Best Local Similarity RESULT 1070
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ID AAZ0948
                                                                     Best Local Similarity
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RESULT 1066
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RESULT 1065
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Mouse fibroblast gro
US6265632-B1.
24-JUL-2001.
                                                                                                  tcp gene cluster.
                            ACN44380 standard; DNA; 76846 BP.
Mouse genomic sequence mCG18525.
WQ2003073826 A2.
12-SEP-2003.
                                                                                                            ADS73531 standard; cDNA; 73882 BP.
                                                                                                                                                                       Human genomic sew
WO2003073826-A2.
                                                                                                                                                                                                                                                                                             ADR66967 standard; DNA; 34571 Mouse cancer associated gene (
                                                                                                                                                                                                                                                                                                                                                                ABL33718 standard; DNA; 17934 BP. Human immune system associated ge WO200200928-A2.
                                                                                                                                                                                            ACN44230 standard;
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                     (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                                                                                                                                        (YEDA) YEDA RES & DEV CO LTD.
(PROC-) PROCHON BIOTECH LTD.
TY Match 2.4%; S
t Local Similarity 51.2%; P
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(KERJ ) FORSCHUNGSZENTRUM JUELICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine carcinoma associated (CA) nucleic acid #56.
US2004072154-A1.
15-APR-2004.
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Bovine retina Ih ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cd; cDNA; growth f.
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on channel
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57.1%;
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DB 11;
5.5e+02;
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.2e+02;
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.7e+02;
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.4e+02;
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.7e+02;
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.8e+02;
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.1e+02;
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2e+02;
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         Length 76846;
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RESULT 1078
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(CHEI/) CHEIKH N.
(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                     ABX40527 standard; cDNA; 3'
Bovine EST associated with
                                                                                                                                                                                                                                                                                  Maize gene confe
WO2003000906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2003.
(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY INCUBAT
                                   Human foetal bra
US2003073623-A1.
                                                                                                         Human soft tissue sarcoma-upregulated WO2004048938-A2.
                                                                                                                            ADQ19577 standard; DNA; 393
                                                                                                                                                                                                                                                                                          ADA49273 standard; DNA; 339 BP.
Maize gene conferring disease resistance in
                                                                                                                                                                                                                                                                                                                                                                           Maize sucrose synthase
US2003135870-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC86916 standard; DNA; 349989 BP.
Human GPCR gene SEQ ID NO:1369.
                                                     ACH44942 standard; cDNA;
                                                                                                                                                                                                            JS2002137139-A1.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                             ADA58541 standard; cDNA;
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDA58745 standard; cDNA;
                                                                                                                                                               WARR/) WARREN W C.
                                                                                                                                                                                                                                                                 SYGN ) SYNGENTA PARTICIPATIONS AG
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/) MATHIALAGAN
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DRMANAC R T.
LABAT I.
STACHE-CRAIN B.
                                                                      PROTEIN DESIGN LABS INC.
h 2.4%; Scc
Similarity 50.3%; Pre
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                                            brain cDNA #5667.
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45.5%;
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55.3%;
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EST #330.
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                                                    487 BP.
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Best
RESULT
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RESULT 1084
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Best Local Similarity
RESULT:1080
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RESULT 1085
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Pseudomonas ae
US6551795-B1.
22-APR-2003.
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(RANK/) RANK D R.
(HANZ/) HANZEL D F
                                                                                                ADM47892 standard; DNA; Polynucleotide sequence US2003233670-A1.
                                                                                                                                                               ADP28033 standard; DNA; 1176 BP. Human secreted protein encoding WO2004035732-A2.
29-APR-2004.
                                                                                                                                                                                                                                                                                  ADT43885 standard; cDNA; 870 BP. Bacterial polynucleotide #18636. US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                         cDNA encoding novel WO200166689-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                ADA68731 standard; DNA;
Rice gene, SEQ ID 2054.
WO2003000898-A1.
                         ABD08729 standard; DNA; 1488
                                                                                                                                                                                                                                                                                                                                                                            AAS44974 standard;
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07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA clone
                                                            (CHOM/) CHOMET P S. (LACC/) LACCETTI L
                                                                                                                                                       (FIVE-) FIVE PRIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome derived single US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JONE/) JONES L W.
                                                                                                                                                                                                                                       (HINK/) HINKLE G
(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                             (SYGN ) SYNGENTA PARTICIPATIONS AG
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                andard; DNA; 1488 BP.
aeruginosa polynucleotide #7333
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(3'-primer)
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47.8%;
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47.5%;
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65;
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78;
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51;
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Best Local Similarity
RESULT 1095
ID ADJ79057 standard; DI
DE Human NOVX protein N:
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERH/) ZERHUSEN B D
PA (ZERH/) ZERHUSEN B D
PA (KEKU/) KEKUDA R.
PA (KEKU/) KEKUDA R.
PA (RIEG/) RIEGER D K.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENA C E A.
PA (PENA/) SHIMKETS R A
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
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RESULT 1093
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                                                                                                                                                                                                                                                          ADE47787 standard; DNA
Human NOV45e gene SEQ
WO2003076642-A2.
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WO2004035732-A2.
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Human cDNA differentially expressed in a liver US2003108871-A1.
                                                                                                                                                                                                 ADH41894 standard; DNA;
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22-APR-2003.
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Pseudomonas aeruginosa polynucleotide
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Human polynucleotide
WO200164835-A2.
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(HYSE-) HYSEQ INC.
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(CURA-) CURAGEN CORP.
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CY Match 2.4%; Score
Local Similarity 50.3%; Pred.
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KEKUDA R.
MILLER C E.
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protein encoding
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Nov45E
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SEQ ID NO:149.
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Best Local Similarity
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Best Local Similarity
RESULT 1096
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                                                    Human macrophage stimulating WO200233087-A2. 25-APR-2002.
Human cDNA encoding US2003212256-A1.
                                                                                                                              ABT08324 standard; DNA; 2011 Human NOV7 gene sequence.
                                                                                                                                                                                    Human equine herpesvirus p24 homologue-encoding W0200157188-A2.
               ADJ38433 standard; cDNA;
                                                                                                                13-JUN-2002
                                                                                                                       Human NOV7 gene WO200246408-A2.
                                                                           ABS59330 standard; DNA; 2011
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Human cDNA sequence SEQ ID NO:16827.
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HJALT T.
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CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINGER S R.
EISEN A J.
GANGOLLI E A.
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GUO X S.
ANDERSON D
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BURGESS C E.
KHRAMTSOV N
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CASMAN S J.
VOSS E Z.
BOLDOG F L.
PADIGARU M.
SMITHSON G.
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RASTELLI L.
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le+02;
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99;
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94;
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Best Local Similarity
RESULT 1105
ID AAD26582 standard; c
DE Human MSP precursor-
PN W0200185767-A2.
PD 15-NOV-2001.
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RESULT 1106
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RESULT 1103
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(HINK/) HINKLE G J.
(SLAT) SLATER S C.
(CHEN) CHEN X.
(GOLD/) GOLDMAN B S.
                                                                                                                                                         AAD26582 standard; cDNA; 2200 BP. Human MSP precursor-like protein, POLY13 encoding WO200185767-A2.
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WO200229058-A2.
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DNA encoding novel hepatoctye
WO200229058-A2.
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ADE47779 standard; DNA; 2200 BP.
Human NOV45a gene SEQ ID NO:141.
WO2003076642-A2.
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GERLACH V.
MACDOUGALL J R.
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SPYTEK K A.
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FERNANDES E R
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PADIGARU M.
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ZERHUSEN B D.
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PEYMAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITHSON G.
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                                                                            DB 6;
1.1e+02;
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1.1e+02;
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1.1e+02;
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1.1e+02;
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le+02;
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1e+02;
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Query Match
Best Local Similarity
RESULT 1110
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Best Local Similarity
RESULT 1109
                                                                                                    Best Local Similarity RESULT 1108
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                                       AAS83814 standard;
DNA encoding novel
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                        Human NOVX protein Nov45A gene sequence.
US204014053-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003102159-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH41896 standard; DNA; Novel human nucleic acid
ACN41132 standard; cDNA; 2533 BP
                          (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2003
                                                                                (SHEN/)
                                                                                             (TAUP/)
                                                                                                                                (DIPI,
(EDIN,
(EISE,
(GANG,
(GIOT,
                                                                                                                                                                                                                                    (SPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-)
                                                                                                                                                                                                                                                                                                                           BERG/
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                                                                               LIU X.
TAUPIER R J.
CATTERTON E.
SHENOY S G.
                                                                                                                GIOT L.
OOI C E.
ROTHENBERG
SPADERNA S
                                                                                                                                          ELLERMAN K.
RASTELLI L.
AGEE M L.
CHAUDHURI A.
CHANT J S.
DIPIPPO V A.
EDINIGER S R.
BISEN A J.
GANGOLLI E A.
                                                                                                                                                                                                              GERLACH V.
BURGESS C E.
KHRAMTSOV N V.
                                                                                                                                                                                                                                                                                 BERGHS C.
ZHONG M.
CASMAN S J.
VOSS E Z.
BOLLDOG F L.
PADIGARU M.
SMITHSON G.
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MILLER C E.
RIEGER D K.
PENA C E A.
SHIMKETS R A.
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PATTURAJAN
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VERNET C !
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                                              cDNA; 2296 BP.
human diagnostic
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No.
                                              protein #19618
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1.1e+02;
                                                                  DB 12;
1.1e+02;
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1.1e+02;
              1.1e+02;
                    DB 5;
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Human NOVX protein
WO2003057854-A2.
ADC86968 standard; I
Human GPCR gene SEQ
EP1270724-A2.
                                                                                                                                                                                                           Human NOVX protein WO2003057854-A2.
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Human NOVX protein
WO2003057854-A2.
                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human diagnostic WO2004023973-A2.
                                                                                                                                          ADP13461 standard; DNA; 6008 BP.
Renal cell carcinoma differentially
                                                                                                                                                                                                                                                                  17-JUL-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                  WO2004048933-A2.
                                                                                                                                                                                                                            ADK18367 standard;
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                            HYSE-) HYSEQ INC.
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                                                   DORNER A.
) STOVER J A.
) SLONI D K.
                                                                                 TWINE N C.

BURCZYNSKI

TREPICCHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN DESIGN LABS INC.
th 2.4%; Score
Similarity 44.3%; Pred.
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                                   Similarity
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encoding
        DNA; 6269 BP.
) ID NO:1421.
                                                                                   ΣZ
                                                                                                                                                                                                                             DNA;
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                                                                                                                                                                                                                                                                                                                                                                       cDNA; 5635 BP. human diagnostic
                                                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding gene #9
                                                                                                                                                                     2.4%;
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                                                                                                                                                                                                                  gene
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                                   Score
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1.7e+02;
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1.7e+02;
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1.6e+02;
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1.4e+02;
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1.1e+02;
                                    DB 12;
1.8e+02;
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1.8e+02;
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.2e+02;
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Query Match
Best Local S
RESULT 1119
ID AAL05754
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RESULT 1123
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RESULT 1120
                                             Mouse genomic sequence WO2003073826-A2.
                                                                                                                                                                                 Human nervous system WO200159063-A2.
                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
xy Match 2.4%;
t Local Similarity 59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                           (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBAT STY Match 2.4%; Score 35; DB 10; L Local Similarity 48.7%; Pred. No. 2.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GPCR gene SEQ EP1270724-A2.
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ry Match 2.4%;
it Local Similarity 59.6%;
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
2.4%; SCOTE 35, DB 10; I
1t Local Similarity 46.8%; Pred. No. 1.8e+02;
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                         ABA20363 standard;
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(ECOP-) ECOPIA BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                              WO2004065401-A1.
                                                                                                                                                                                                                                                                                                                                                                                        ADQ91701 standard; DNA; 10287 BP. Polyketide synthase ORF11, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC86850 standard; DNA; 8360 BP.
Human GPCR gene SEQ ID NO:1303.
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14-AUG-2003.
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                                                                     CN44588 standard;
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2.4%;
Similarity 51.6%;
                        SAGRES DISCOVERY
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em related poly
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No.
DB 11;
4.1e+02;
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2.3e+02;
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2.9e+02;
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2.9e+02;
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1.9e+02;
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1.9e+02;
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1.9e+02;
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DB 10; Length 8360;
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3.5e+02;
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Best Local Similarity
RESULT 1134
ID ADC85227 standard; Di
DE Mouse Irf2 genomic so
PN w02003045230-A2.
PD 05-JUN-2003.
                                                                                                           RESULT
ID AL
DE MU
PN US
PD 15
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Best Local Similarity
RESULT 1130
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                                       ADN30326 standard; DNA; 121434 BP.
Human Notch2 genomic DNA region #1
US2004101847-A1.
                                                                                                                                          ADM74342 standard; DNA; 96599 Murine carcinoma associated (C
                                                                                                                                                                                                                                                                                            ADB72485 standard; DNA; 96599 Mouse Irf2 gene. W02003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse genomic sequence mCG19337. W02003073826-A2.
                                                                                                                               Murine carcinoma
US2004072154-A1.
                                                                                                                                                                                                             Mouse Irf2 genomic sequence. WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN44064 standard; DNA; 44748 BP Mouse genomic sequence mCG13520. WO2003073826-A2.
                                                                                                                                                                                                                                 ADC85227 standard; DNA; 96599
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                                                                                                                                                                                                                                                                                                                                                                                        Mouse Irf2 carcinoma associated
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ry Match 2.4%;
Local Similarity 54.2%;
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(SAGR-) 2.4%;
CY Match 2.4%;
c Local Similarity 47.9%;
                                                                                                 (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
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etic antigen
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DB 12;
7.8e+02;
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5.6e+02;
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5.4e+02;
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4.8e+02;
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7e+02;
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7e+02;
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7e+02;
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Query Match
Best Local Similarity
RESULT 1144
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                                                                                                                                                                                                              Human secreted protein 5'
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WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse cancer ass
WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyketide synthase related DNA contig
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                                                                                          (ANYY/)
                                                                                                                              US2002040489-A1.
                                                                                                                                      ABX56967 standard; DNA;
Arabidopsis thaliana pol
                                                                                                                                                                                                                         AAC10054 standard; cDNA; 530
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                                                                                                                                                                                                                                                                                        Human polynucleotide
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ry Match 2.4%;
t Local Similarity 30.6%;
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                                                                                                                                                                                     (GEST ) GENSET.
                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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ry Match 2.4%;
t Local Similarity 57.9%;
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                          PAGE A.
MATHEW A V.
LEDFORD B L.
                                                                      HAMILTON C N
PRICE J L.
RAINES T M.
                                                                                                                                                                                                                                                                                                                   SYNGENTA PARTICIPATIONS AG. h 2.3%; Score Similarity 48.9%; Pred.
WOESSNER J P. HAAS W D. GARCIA C A.
                                                                                                            GORLACH J.
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                                                      RAMEAKA J G.
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associated
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4010.
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de SEQ
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57.9%;
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(CA) gene
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sequence MD08-038,
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ID NO 2179
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No. 60;
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8.8e+02;
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Lest Local Rest Local RESULT 1149
ID AAI70°
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Best Local S
RESULT 1146
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Best Local Similarity
RESULT 1145
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Best Local |
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                                                                  03-JAN-2003.
03-JAN-2003.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
317 Match
2.3%; Score
317 Match
48.9%; Pred.
                                            AAX90405 standard; DNA; 1375
Actinomadura sp. DSM43186 35
                                                                                                            WO2003000906-A2.
                                                                                                                    ADA49077 standard; DNA; 1290 BP. Wheat gene conferring disease re
                                                                                                                                                                                       WO200192485-A1.
                                                                                                                                                                                              Rat histamine H4 receptor
                                                                                                                                                                                                         AAI70982 standard;
                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide WO200171042-A2.
                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID EP1033405-A2.
                                                                                                                                                                                                                                                                                                                   06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                              AAC39827 standard;
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(INCY-) INCYTE CORP
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Human steroid-induced C3A
                                                                                                                                                                  (ORTH ) ORTHO-MCNEIL PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant cDNA #3637.
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(DAVI/)
(ALLE/)
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Local Similarity
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1148
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KATAGIRI F.

KREPS J.

PROVART N.

RICKE D.
ROEHM ENZYME FINLAND h 2.3%; Similarity 49.5%;
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                                                                                                                                                                                                                                                                                   ZHU T.
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                                                                                                                                                                                              cDNA; 1176 B
eceptor cDNA.
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34.8;
No. 96;
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No. 93;
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No. 89;
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No. 80;
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No. 71;
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No. 71;
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No. 69;
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No. 62;
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                                                                                                                                                                                                                                                                                                          751;
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Best Local Similarity
RESULT 1160
ID ADT45909 standard; c
DE Bacterial polynuclec
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 1159
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Best Local Similarity
RESULT 1157
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RESULT 1153
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DAT64950 standard; DNA; 1375

DE Actinomadura flexuosa 35 kDa

PN W09727306-A1.
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                                                                                                             DNA encoding novel 1 W0200175067-A2. 11-OCT-2001. (Hyss-) HyssQ INC.
                           Bacterial polynucleotide US2003233675-A1.
18-DEC-2003.
                                                                                                                                                            AAS83500 standard;
                                                                                                                                                                                                                               Human cDNA encoding EP1308459-A2. 07-MAY-2003.
                                                                                                                                                                                                                                                                                                                                   ACA27342 standard; DNA; 2028 BP. Prokaryotic essential gene #8999. W0200277183-A2.
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21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
2.3%;
ery Match
2.3%;
57.3%;
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                                                                                                                                                                                                                                                    ADB63067 standard; cDNA; 2077
Human cDNA encoding clone SMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel
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WO200277183-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS68016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FIVE-) FIVE PRIME THERAPEUTICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD035997 standard;
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                                                                                                                                                                                                                                                                                                              ELITRA PHARM
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                                                                                                                                                cDNA;
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equence #670.
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2.3%;
49.5%;
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60.6%;
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human diagnostic
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SMINT20007470
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Pred.
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(AM35) xylanase encoding
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No. 1.3e+02;
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No.
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.2e+02;
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.2e+02;
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.1e+02;
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Query Match
2.3%;
Best Local Similarity 49.5%;
RESULT 1161
ID AAS56030 standard; DNA; 2679
DE Salmonella typhi DNA for cell
PN WQ200170955-A2.
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Best I
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Best Local Similarity
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                                                                                                            06-MAY-1999.

06-MAY-1999.

(MASI ) MASSACHUSETTS INST TECHNOLOGY.

2:3%; Score 34.8;

2:7 Score 34.8;

3:7%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                    Bacterial polynucleotide US2003233675-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ23911 standard; DNA;
Human 3OST4 polypeptide
WO200292849-A2.
                                          Human nervous system WO200159063-A2.
                                                   ABA16206 standard; DNA; 4034
Human nervous system related
                                                                                                                            WO200159063-A2.
                                                                                                                                       Human nervous
                                                                                                                                                                                                              AAX37250 standard; DNA; 3658
Human 3-OST-4 encoding DNA.
WO9922005-A2.
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ry Match
Local Similarity 50.6%; Pred.
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(ASTR ) ASTRAZENECA UK LTD.

ry Match 2.3%;

t Local Similarity 53.7%;
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                                                                                                                                     ABA15504 standard; DNA; 4034 duman nervous system related
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h 2.3%;
Similarity 58.8%;
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Ce 34.8;
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.5e+02;
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.3e+02;
 DB 5;
.6e+02;
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.6e+02;
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.4e+02;
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Query Match
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RESULT 1174
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RESULT 1177
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RESULT 1176
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RESULT 1175
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RESULT 1173
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RESULT 1171
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RESULT 1170
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AAX37551 stanua...
Human 3-OST-4 5' promoter ...
# W09922005-A2.
D 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
AMATCh 2.3%; Score 34.8;
MASICh 31-rity 53.7%; Pred. No. 1.
                                                                                                                                                Query Match
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                                                                                                                                                                                Human 3OST4 gene
WO200292849-A2.
21-NOV-2002.
                                                                                                                                                                                                                                                                       AAQ04668 standard; DNA; 12036 BP.
FHA Structural gene, fhaB.
WO9004641-A.
03-MAY-1990.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                          (INRM ) INSERM INST NAT SANTE 2.3%; St Local Similarity 49.5%; I
                                                                                                FMR2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human respiratory US2003215893-A1. 20-NOV-2003.
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Human digestive
WO200155314-A2.
                     AAK89020 standard; DNA;
                                                                            WO9967395-A1.
29-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA10263 standard; DNA; 11883 BP.
Bordetella pertussis filamentous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory US2003077704-A1.
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                                                                                                             ABN97984 standard; DNA; 13695
                                                                                                                                                                                                                 ABZ23912 standard;
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ry Match 2.3%;
t Local Similarity 57.3%;
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DOMENIGHINI
RAPPUOLI R.
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system associated polypeptide-related DNA SegID1024.
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system associated
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Score 34.8; DB 3;
Pred. No. 3e+02;
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          genomic
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No.
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No.
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No. 1.7e+02;
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.7e+02;
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.7e+02;
                                                                                                                                    DB 8;
.9e+02;
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.8e+02;
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.8e+02;
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.6e+02;
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           SEQ
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02-AUG-2001

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Best Local Similarity
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RESULT 1184
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RESULT 1178
             Query Match
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                                                                                                                                                                                                       Human colorectal cancer related polypeptide DNA US2003054420-A1.
                                          WO9911799-AZ.
                                                     Human kidney
                                                               AAX23520 standard;
                                                                                                                            WO200157182-A2.
                                                                                                                                   AAK66362 standard; DNA; 3693
Human immune/haematopoietic
                                                                                                                                                                                     20-MAR-2003.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                               ADB32581 standard; DNA; 32152 BP.
Human novel colon related polypeptide DNA
US2003050231-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                    ABS99968 standard; DNA; 32152 BP.
Genomic DNA #172 encoding human colorectal
US2002119919-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence WO200155302-A2.
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Human colorectal ca
WO200155350-A1.
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Human digestive system antigen genomic
W0200155314-A2.
                                11-MAR-1999
                      (MEDI-)
                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS39621 standard;
                                                                                                                                                                                                                                                                                                                                                                           (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                    Local Similarity
MEDICAL COLLEGE GEORGIA RES INST.

1. 2.3%; Score 34.8;
Similarity 54.8%; Pred. No. 5.
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#40 encoding
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                                                   DNA; 45546
peptidase P
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2.3%;
55.9%;
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Pred.
 Score 34.8; DB 2;
Pred. No. 5.5e+02;
                                                   BP.
genomic
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human
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5.5e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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Best Local Similarity
RESULT 1196
ID ACN44002 standard; D
DE Human genomic sequen
PN W02003073826-A2.
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RESULT 1187
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RESULT 1192
Query Match
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                                                                                               ADL13775 standard; DNA; 173805 BP. Osteoarthritis-associated polymorphic WO2003054166-A2.
                                                                                                                                                                                            ABD33312 standard; DNA; 138115 BP. Murine cancer-associated (CA) gene W02004058146-A2.
          ACN44002 standard; DNA; 228139 BP
Human genomic sequence hCG37533.
                                                                                                                                                                                                                                             (PROT-) PROTEIN DESIGN LABS INC.
ry Match 2.3%; Score
Local Similarity 54.8%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse genomic se WO2003073826-A2.
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Mouse cancer associated sequence MD08-035, W02204060304-A2.
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                                                                                                                                                                                                                                                                                                                      ADQ17592 standard; DNA; 116561 BP
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ry Match 2.3%;
t Local Similarity 53.7%;
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WO2003073826-A2.
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2.3%; Score 34.8;
tt Local Similarity 50.6%; Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            L2-SEP-2003
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                                              INCYTE GENOMICS INC. h 2.3%; Similarity 53.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence mCG12182.
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No. 9
                                                34.8; DB 10
No. 1.1e+03;
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5.9e+02;
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.4e+02;
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.7e+02;
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.5e+02;
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.5e+02;
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'.9e+02;
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.9e+02;
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.3e+02;
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MOLECULAR .

LUCI MATCH

Best Local Similarity

RESULT 1205

ID ABS28139 stapa-

DE Human liv-

PN WO20-
                                                                       MOLECULAR.

Meet Local Similarity

RESULT 1204

ID AAK03087 stand

DE Human brain

PN WO200
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RESULT 1199
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                                                                                                                                                             Human bone marrow WO200157276-A2.
                                                                                             Human brain expressed single exon
                                                                                                       AAK03087 standard; DNA; 422
                                                                                                                                                                                AAK28539 standard;
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                                                                                                                                                                                                                                                        ABA24575 standard; DNA; 422
                                                                                                                                                                                                                                                                                                               Human breast cell single exon nucleic WO200157271-A2.
                                                                                                                                                                                                                                                                                                                                                                                        WO200157272-A2.
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Human foetal liver single exon nucleic
WO200157277-A2.
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Probe #3045 for gene express
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SSG #9.
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                                               JE-) MOLECULAR DYNAMICS INC.
fatch 2.3%; Score
cal Similarity 64.2%; Pred.
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h 2.3%; Score
Similarity 64.2%; Pred.
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h 2.3%;
Similarity 48.1%;
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                     DNA; 422 BP. exon probe,
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Query Match
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RESULT 1208
                                     Best Local Similarity RESULT 1213
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RESULT 1211
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RESULT 1209
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Zea mays DNA fragment SEQ
EP1033405-A2.
Pseudomonas aeruginosa polynucleotide #2298
US6551795-B1.
22-APR-2003.
                                                                                     Human GPCR gene, WO2003000893-A2.
                                                                                              Human GPCR
                                                                                                                                                                                                                                                                                                                         07-NOV-2002.
(UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                            ABZ22262 standard; DNA; 615 BP. Schwann cell specific enhancer consensus WO200288352-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single WO200186003-A2.
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                                                                                                        ADC12755 standard;
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WO2003000898-A1.
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ry Match 2.3%
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                             ABD03694 standard;
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US2004016025-A1.
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KREPS J.
PROVART N.
                                                                                                                                                                                            BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
COOPER B.
GLAZEBROOK J.
GOFF S A.
                                             DECODE GENETICS EHF.
h 2.3%;
Similarity 53.3%;
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ZHU T.
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h 2.3%; Score
Similarity 47.1%; Pred.
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SEQ ID
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No. 90;
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Best Local Similarity
RESULT 1218
ID ABS7777
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ID ADB4764
DE Human c
PN US20031
PD 10-JUL-
PA (FEDE/)
PA (RAMA/)
PA (HAWK/)
 Best Local Similarity
RESULT 1219
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RESULT 1216
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RESULT 1217
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RESULT 1215
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Human GPCR 14273 coc
WO2004065960-A1.
05-AUG-2004.
                                                                                                    (FEDE/) FEDER J N.
(MINT/) MINTIER G.
(RAMA/) RAMANATHAN C
(HAWK/) HAWKEN D R.
                                                                                                                                                                                                                                                                                                                      cDNA encoding human GPCR HF1948. WO200268600-A2.
                                              Human G-protein
US2004161823-A1.
                                                                                                                                                    Human cDNA encoding US2003129653-A1.
                                                                                                                                                                                                                                                  CDNA encoding novel US2003022186-A1
                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human GPCR WO200268600-A2.
06-SEP-2002.
(AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABT04869 standard; cDNA; 1086 BP. Human G protein coupled receptor hRUP31 coding W0200242461-A2.
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ry Match 2.3%;
t Local Similarity 53.3%;
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(UYMC-) UNIV MCGILL.
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Mouse and human consensus SCE1 nucleotide sequence
WO200288352-A2.
                                                                 ADR40535 standard; cDNA;
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Human cDNA encoding GPCR, HGPRBMY18.
                                                                                                                                                                                                                                                                     ACA60998 standard;
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ry Match
2.3%;
t Local Similarity 53.3%;
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(MINT/) MINTIER G.
(RAMA/) RAMANATHAN
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                             FEDE/)
                                      9-AUG-2004.
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FEDER J N.
) MINTIER G.
) RAMANATHAN (
) HAWKEN D R.
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HF1948 m
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Best Local S
RESULT 1226
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RESULT 1223
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Best Local Similarity
RESULT 1229
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RESULT 1225
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Best Local Similarity
RESULT 1224
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

2.3%; Score 34.6; DB 10;

PTY Match

2.3%; Pred. No. 1.1e+02;
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                                                                                                    ADR01275 standard; DNA; 1599 BP.
Farnesyl dibenzodiazepinone biosynthetic
                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK.
xry Match 2.3%;
t Local Similarity 53.3%;
                                                                                                                                                                                                AAI66039 standard; cDNA; 1458 BP.
Human G protein-coupled receptor
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US2002151705-A1.
17-OCT-2002.
DNA encoding a WO200050596-A2.
                       AAA64346 standard; DNA; 1743
                                                                                            WO2004065591-A1.
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Human GPCR gene SEQ ID NO:1833.
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ry Match 2.3%;
t Local Similarity 53.3%;
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Bacterial polynucleotide
US2003233675-A1.
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                                                                  (ECOP-) ECOPIA BIOSCIENCES INC.
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(SLAT/) SLATER S
(CHEN/) CHEN X.
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nan SNORF49
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          coupled
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No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 1e+02;
                                              34.6;
No. 1.
                                                                                                                                          34.6; DB 4;
No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                         34
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
No
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1.6
          receptor designated 14273.
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                                              DB 13;
.2e+02;
                                                                                                                                                                                                                                                                                                                                         DB 13;
.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
.1e+02;
                                                                                                       ORF32
                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
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                                                                                                     protein
                                                                                                                                                  Length
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Best Local Similarity
RESULT 1236
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                                                  Best Local Similarity RESULT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                BBBB
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1233
                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB53747 standard; DNA; Primary rat hepatocyte t WO2003065993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADF70511 standard; DNA; 1800 BP. Orphan receptor ligand-related h WO2003071272-A1.
                                                                                                                                                                                           ADA70561 standard; DNA; Rice gene, SEQ ID 3884. WO2003000898-A1.
                    EP1308459-A2.
                                                                                                       Prokaryotic essential gene WO200277183-A2.
                                                                                                                              ACA50840 standard;
                                                                                                                                                                                                                                                                                 WO2004040000-A2.
                                                                                                                                                                                                                                                                                          ADO28989 standard; cDNA; 2081 BP.
Human novel GPCR PGR4 polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                            ABD11675 standard; DNA; 2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE ) GENE LOGIC INC.

2.3%;

ry Match 2.3%;

t Local Similarity 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003064624-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB58993 standard; DNA;
Toxicity-related gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
ry Match 2.3%;
t Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200267868-A2.
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                                         ADB63556 standard;
                                                           (ELIT-) ELITRA PHARM INC.
ry Match 2.3%;
t Local Similarity 46.5%;
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                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG

CY Match 2.3%; Score

: Local Similarity 49.2%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD.
ry Match 2.3%;
Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                              Match 2.3%; ocal Similarity 51.6%;
                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                            ocal Similarity
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                                                                                                                                                                                                                                                          PRIMAL INC.
HELIX RES
                              encoding
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c acid, associated with metabolic
                                                                                                                             DNA;
                              clone
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                                                                                                                                                                                                                                                                                                                                                                                ; 2073 BP.
polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2034 BP.
toxicity modelling
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SEQ ID
                                                                                                                  2355 BP.
ene #32497.
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                              2650 BP.
e TESTI20287760
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No. 1.
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No.
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No. 1.
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No. 1.2e+02;
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No. 1.
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No.
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                                                                                                                                                                                                                                      DB 12;
.3e+02;
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.3e+02;
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.3e+02;
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.3e+02;
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.4e+02;
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.2e+02;
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Query Match
Best Local S
RESULT 1241
                                                                                 Best Local Similarity RESULT 1246
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RESULT 1242
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Best Local Similarity
RESULT 1239
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                                                   AAA10594 standard; DNA;
Gene encoding a subunit
JP2000060568-A.
                                                                                                                                   ADR01273 standard; DNA; 5960 Farnesyl dibenzodiazepinone l WO2004065591-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IBAR-) IBARAKI PREFECTURE.
xry Match
t Local Similarity 56.6%;
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Pseudomonas aeruginosa polynucleotide #10577
                                                                                                                                                                                                                                                                                                                                                        AAL51404 standard; cDNA; 3537
Human secreted protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004048938-A2.
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Human gene sequence #3.
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                                                                                                                                                                                                                                                                                   (BEAS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ23587 standard; DNA; 3141
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(PROT-) PROTEIN EXPRESS CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene sequence
W0200299103-A1.
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                                                                                                                                                                                                                                                                                                       GONG/)
                                                                                                                                                                           ocal Similarity
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                    ) OJI PAPER
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th 2.3%;

Similarity 56.6%;
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 Similarity
                                                                                                              ECOPIA BIOSCIENCES
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DI FRANCESCO V.
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132
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                                                               10732 BP.
of cellulose
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k; Score
k; Pred.
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Pred.
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sequence,
No. 3e+02;
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No. 1.
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.6e+02;
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.5e+02;
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.3e+02;
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.8e+02;
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.8e+02;
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.7e+02;
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.6e+02;
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RESULT 1247
ID AAS5956
DE Propion
PN WO20018
PD 01-NOV-
PA (CORI-)
                                                                                                     Dest Local Similarity
RESULT 1254
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BRBB
                                 Best Local Similarity RESULT 1255
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RESULT 1250
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                                                    Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse cancer-associated WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS59569 standard; DNA;
Propionibacterium acnes
WO200181581-A2,
01-NOV-2001.
      Human DNA sequence WO200151659-A2.
                          AAH88704 standard;
                                                                             ADQ97700 standard; DNA; Mouse cancer associated WO2004060304-A2.
                                                                                                                                                                               US2002052034-A1.
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                                                                                                                                                                                                                                                                     ABD33307 standard; DNA; 53828 Murine cancer-associated (CA)
                                                                                                                                                                                                                                                                                                                                   WO2003099993-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Full length
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                                                                                                                                                                                               Human lipase encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.3%;
t Local Similarity 54.3%;
                                                                                                                                                                                                         ABN87364 standard;
                                                                                                                                                                                                                                          (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                              (AVET ) AVENTIS PHARM INC.
ry Match 2.3%;
t Local Similarity 54.3%;
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                                                                                                                                                    ) GUEGLER K.
) WEBSTER M.
) KETCHUM K A.
                                         SAGRES DISCOVERY INC. h 2.3%; Similarity 50.9%;
                                                                                                                                   BEASLEY
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BEASLEY E M.
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               DNA; 160755 BP
SEQ ID 544.
                                                                                                                                                                                                        cDNA; 55155
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2A7.
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50.9%;
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2.3%;
54.3%;
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sequence
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genomic DNA
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No. 6.
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No. 5.
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No. 5e+02;
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No.
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No. 6.
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.8e+02;
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.4e+02;
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Best Local Similarity RESULT 1264
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RESULT 1259
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RESULT 1257
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                                                                   Alternatively spliced form of WO200129235-A2.
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Human target of methylation-induced
W0200129235-A2.
26-APR-2001.
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Human colon cancer WO200055351-A1.
                  AAC98638 standard;
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Human genomic sequence hCG38337.
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                                                                                                                                                                      ADE09716 standard;
                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                        (UYEM-) UNIV EMORY
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Similarity 53.3%;
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56.8%;
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Pred. No. 60;
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No. 1.
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68;
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66;
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.5e+03;
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HUMAN

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RESULT 1272
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RESULT 1273
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Best Local
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                                                                     ABS56032 standard; cDNA; 740 BP. cDNA encoding human caspase recr
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CpG island of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC36571 standard; DNA; 4 Arabidopsis thaliana DNA
Human novel cytokine
WO200175093-Al.
              AAS59817 standard;
                                                                                                                             Human caspase recruitment WO200244354-A2.
                                                                                                                                             ABK87967 standard;
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WO200244354-A2.
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Human CARD-5 cDNA.
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WO200129235-A2.
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Bovine EST associated with lactation/muscle/fat
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                                               (BERT/) BERTIN J.
                                                                                                                                                                            (MILL-) MILLENIUM
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(MATH/) MATHIALAGAN
(TAON/) TAO N.
                                                       2-SEP-2002
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Similarity 46.0%;
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No. 92;
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No. 70;
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No. 84;
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CDNA

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Best Local
RESULT 1282
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Best Local Similarity
RESULT 1280
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RESULT 1279
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RESULT 1275
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                                                                                                                                                                                                                                                                                 Human colon cancer antigen encoding WO200122920-A2. 05-APR-2001.
                                                                                                                                     ADR01252 standard; DNA; 825
Farnesyl dibenzodiazepinone
WO2004065591-A1.
05-AUG-2004.
                                                                                                                                                                                                                     Human cancer associated gene WO200055350-A1.
                                                                                                                                                                                                                                         AAC77884 standard;
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Human TMS1 DNJ
DE10255104-A1
                  ADP07316 standard;
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WO2004028479-A2.
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                                                                                         ADN05025 standard;
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h 2.3%;
Similarity 54.8%;
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tumour-associated |
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                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rd; cDNA; 770 BP. methylation-induced
                                                                               cDNA; 936
sequence #
                                                                                                                                                                                                                                                                                                                                                                                                         S & DEV LTD.
2.3%; S
46.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S GENOMFORSCHUNG
2.3%; Score
46.0%; Pred.
                  DNA; 936
                                                                                                                                                                                                                                         CDNA; 811
                                                                                                                                                                                 2.3%;
46.0%;
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46.0%;
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46.0%;
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46.0%;
                                                                                                          ; Score
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#727
                  ВP
                                                                                                                                                       BP.
biosynthetic
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
                                                                                                                                                                                                                               sequence
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34.4;
No. 9
                                                                                                                                                                                                                                                           34.4;
No. 96;
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No. 93;
                                  34.4;
No. 16
                                                                                                          34.
No.
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No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                           34.4;
No. 94;
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No. 92;
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No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        silencing-1
                                                                                                      4.4;
97;
                                                                                                                                                                             1.4;
96;
                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                  4; DB
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
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                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                   ВB
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                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                        NO:1134
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                                                                                                                                                        ALDB
                                                                                                                                                                                          811;
                                                                                                                                                                                                                                                                                                                                                                                                                    782;
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                                                                                                                    825;
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Best Local Similarity
RESULT 1287
ID AASTT
                                                              Best Local Similarity RESULT 1290
                                                                                                       PA
PA
PA
PA
PA
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RESULT 1288
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PA
PA
PA
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RESULT 1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
RESULT 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A (CHIB-) CHIBA PREFECTURE.
A (HISM ) HISAMITSU PHARM CO LTD.
Query Match 2.3%; Score
Rest Local Similarity 46.7%; Pred.
                                                                                  Query Match
                                                                                                                                                                                           Query Match
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                              ADC45988 standard; cDNA; 1619 BP. Human neoplastic disease-associated US2003082758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                                                                            Human cDNA encoding US2002168711-A1.
                                                                                                                                                                                                  02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                         WO200155163-A1.
                                                                                                                                                                                                                                 AAS34830 standard; cDNA; 1619 BP. cDNA encoding novel human neoplastic
                                                                                                                                                                                                                                                                                                         AAS27365 standard; cDNA; 1619 BP. cDNA encoding novel signal transduction WO200154733-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeri
WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                     AAS54218 standard; DNA; 1470 BP.
Pseudomonas aeruginosa DNA for cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT46829 standard; cDNA;
Bacterial polynucleotide
US2003233675-A1.
                                                                                           (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                          ADB93543 standard;
                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma WO200166719-A1.
             (HUMA-)
                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
ry Match 2.3%;
t Local Similarity 46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004039956-A2.
13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP56277 standard; cDNA; 936 BP.
Human PRO CDNA sequence SEQ ID NO:2253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI97783 standard; cDNA; 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                     HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                             Match
HUMAN GENOME SCI INC.
                                                                                                                                                           CDNA; 1619
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46.0%;
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                                                                                                                                                 novel
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                                                                                                                                               protein
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Pred.
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Pred.
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Pred.
                                                                                                                                                           BP.
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polynucleotide
34.4;
                                                                                                                                                                              34.4; DB
No. 1.4e+0
                                                                       34.4;
No. 1.
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No. 1.
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No. 1.
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No. 1.
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No. 1
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No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4; DB
No. 1e+02;
                                                                                                                                                #390.
                                         gene
                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; DB 1
1e+02;
                                                                       DB 10;
.4e+02;
                                                                                                                                                                              DB 4;
.4e+02;
                                                                                                                                                                                                                                                               DB 4;
.4e+02;
                                                                                                                                                                                                                                                                                                                   pathway
                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                     proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
..1e+02;
                                         64 cDNA
DB
10;
                                                                                                                                                                                                                                 associated
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                                                                                                                                                                                                                                                                                                                   protein,
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Length 1619;
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                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                          1619;
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                                                                                                                                                                                                                                                                                                                   Seq ID 400.
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RESULT 1291
ID ADF30323 star DE Human -
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Best Local S
RESULT 1294
                              Best Local Similarity RESULT 1297
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RESULT
                                                                                                                Best Local
RESULT 1296
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1293
                                                                                                                                                                                                   Best Local Similarity RESULT 1295
                                                                                                                                   Query Match
                                                                                                                                                                                                                       Query Match
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                                                                               AAS44718 standard;
Human full-length p
WO200164834-A2.
                                                                                                                                                                   Human target of WO200129235-A2.
cDNA encoding no 
US2002132291-A1.
                   ABX14762 standard;
                                                                                                                                                                                       AAD03889 standard; DNA; 2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                            (HYSE-) HYSEQ INC.
                                                                                                                                               (UYEM-) UNIV EMORY.
                                                                                                                                                           26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ50974 standard; cDNA; 2'
Human cDNA encoding NOV15a
US2004030096-A1.
12'-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding US2002168711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS27013 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF30323 standard; cDNA; 2525
                                                                                                                                                                                                                                                                                                                                                 (ZHON/
                                                                                                                                                                                                                                                                                                                                                                                                     (EDIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB93191 standard;
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                                                                                                                                                                                                                                                                 CASM
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                                                                                                                         ocal Similarity
                                                                                                                                                                                                                              PENA C A.

PENA C A.

BURGESS C E.

SCIORE P.

STONE D J.

TAUPIER R J.

CASMAN S J.

ROTHENBERG M E.

MALYANKAR U M.

BOLDOG F L.
                                                                                                                                                                                                                                                                                                                                                                                  PADIGARU M.
GUO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                ZHONG M.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                    ZERHUSEN B D.
EDINGER S R.
                                                                                                                                                                                                                                                                                                                                                                                                                          GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                     KEKUDA R.
        novel
                                                                                          ; DNA; 3321 BP. polynucleotide
                   CDNA; 3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA;
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         human
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2.3%; ;
50.6%; ;
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                                        2.3%;
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        ras-like
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cDNA encoding novel signal transduction pathway protein, W0200154733-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer suppressing protein PP10443-encoding CN1368508-A.
11-SEP-2002.
(SHAN-) SHANGHAI INST ONCOLOGY.
                                                                                                                                                         rd; DNA; 2821 BP.
methylation-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score
52.9%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                             Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
                                                                            sequence
                                                                                                                                                                                    34.4;
No. 1.
protein.
                                                                                                         34.4;
No. 1
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No. 1.
                             34.4; DB 4;
No. 1.9e+02;
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No. 1.
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No. 1.7e+02;
                                                                                                                                                        silencing-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4e+02;
                                                                                                                                                                                    DB 12;
..8e+02;
                                                                                                         DB 4;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
.7e+02;
                                                                             #143
                                                                                                                                                         (TMS1)
                                      Length 3321;
                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                         genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq ID
                                                                                                                                                          DNA.
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METTA IN NETHERLANDS

WHICH

WEST LOCAL SIMILARITY

RESULT 1304

ID ABN95047 stand

DE Gene #1547

PN WO200
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Best
 Query
Best L
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                  Query
                                                                                                                              ABN95047 standard; DNA; 4702 BP.
Gene #1545 used to diagnose liver cancer.
W0200229103-A2.
                                                     Human reproductive
                                                                                                                                                                                                                             ADR24345 standard; DNA; 4670 BP.
Breast cancer prognosis marker #206.
WO2004065545-A2.
                                                   AAL06946 standard; DNA; 12232 BP. Human reproductive system related
                                                                                                                                                                                                                                                                                                                   Human serrate 2 encoding WO9802458-Al.
                                                                                                                                                                                                                                                                                                                                       AAV15181 standard; cDNA to mRNA; 3955
                                                                                                                                                                                                                                                                                                                                                                                                        WO2003066831-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Angiogenesis-differentially
                                                                                                                                                                                                                                                                                                                                                                                                                             ADK65790 standard; DNA; 3438 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTSIG encoding WO2004001005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH61306 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
ry Match 2.3%;
t Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer re
US2003099974-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACN88722 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cancer WO200151628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL26787 standard;
                                                                                              1-APR-2002.
(GENE-) GENE LOGIC INC.
2.
                                                                                                                                                                                                                                                                                                                                                             (ORIG-) ORIGENE TECHNOLOGIES cy Match 2.3%; Local Similarity 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
ry Match 2.3%; Score 34.4; DB
L Local Similarity 52.9%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
                                                                                                                                                                                              (ROSE-) ROSETTA INPHARMATICS LLC.
                                                                                                                                                                                                                                                                      (ASAH ) ASAHI KASEI KOGYO KK.
CY Match 2.3%;
Local Similarity 51.3%;
                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
            Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCYTE CORP
                      HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 3420 BP.
A 7512389CB1,
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                                                                                    2.3%;
51.3%;
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49.4%;
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. No. 2e+02;
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No. 2.
 34.4;
No. 3.
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No. 2.
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No. 2e+02;
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No. 2.
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No. 2e+02;
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No. 2e+02;
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                                                                                                                                                                         DB 13;
.3e+02;
DB 4;
.7e+02;
                                                                                    DB 6;
.3e+02;
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.le+02;
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          Length 12232;
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RESULT 1309
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     Query Match
Best Local Similarity
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WO9724435-A1.
10-JUL-1997.
(DARW-) DARWIN MOLE
                                                                                           O2-JAN-2003.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

2.3%; Score 34.4; DB 10;

ery Match

57.4%; Pred. No. 1.9e+03;
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15-JUL-2004.

(SAGR-) SAGRES DISCOVERY INC.

2.3%;

2.3%;

2.3%;

44.2%;
                                                     Corn seedling-derived US2003237110-A9.
                                                                                                                                                                  ADC86916 standard; DNA; 349989 BP. Human GPCR gene SEQ ID NO:1369. EP1270724-A2.
                                                                                                                                                                                                                (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER
ry Match
2.3%; Score 34
t Local Similarity 53.8%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genomic se WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD33201 standard; DNA; 36312 Murine cancer-associated (CA) WO2004058146-A2.
                                                                               ADS67678 standard;
                                                                                                                                                                                                                                                                        27-OCT-2000.
                                                                                                                                                                                                                                                                                             AAH41223 standard; DNA; 349980 BP.
Pyrococcus abyssi genomic fragment
                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY INC.
ry Match 2.3%;
t Local Similarity 54.8%;
                                                                                                                                                                                                                                                                                                                                                                                    WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                              ADQ97651 standard; DNA; 127943 BP.
Human cancer associated sequence HD10-021,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse genomic sequence WO2003073826-A2.
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ry Match
2.3%; Score
Local Similarity 54.8%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN44818 standard; DNA;
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2.3%;
Similarity 55.0%;
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2.3%; Score
47.6%; Pred.
                            INCYTE PHARM INC.
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                                                                 cDNA; 238 BP.
red polynucleotide
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   2.3%;
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No. 1.
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4.2;
59;
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4.3e+02;
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1.1e+03;
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.9e+03;
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.2e+03;
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.7e+02;
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.4e+02;
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.4e+02;
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RESULT 1315

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LUETY N.
Best Lock
RESULT 1321
ID AAS60
DE DN
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RESULT
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Best Local
RESULT 1317
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Best Local Similarity
RESULT 1319
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RESULT 1
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                                  Rice gene, SEQ I
WO2003000898-A1.
                                         ADA69917 standard;
Rice gene, SEQ ID 3
                                                                                                      WO200175067-A2.
                                                                                                             DNA encoding novel
                                                                                                                      AAS75461 standard;
                                                                                                                                                                         DNA encoding novel WO200175067-A2.
                                                                                                                                                                                                                                             Human ovarian cancer related WO200192581-A2.
                                                                                                                                                                                                                                                                                                              Nucleotide sequence WO200153524-A2.
                                                                                                                                                                                          AAS69547 standard;
                                                                                                                                                                                                                                                             ABL87669 standard; cDNA; 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast
                                                                                                                                                                                                                                                                                                                                AAH42837 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200264611-A1.
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(FINC/) FINCHER K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton expressed US2004123338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP94454 standard; cDNA; Cotton expressed sequence
                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                           26-JUL-2001.
(UYNO-) UNIV NOTTINGHAM TRENT.
                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                             AAF07736 standard;
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SYNGENTA PARTICIPATIONS AG.
h 2.3%; Score
Similarity 54.3%; Pred.
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                                         ; DNA; 978
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2.3%; S
55.5%; P
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e of a
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EST SEQ ID NO
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diagnostic
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human me
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diagnostic
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                                                                   34.2; DB
No. 1e+02;
34.2;
No. 1.
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No. 91;
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No. 1e+
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No.
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No.
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No. 77;
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No. 65;
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97;
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79;
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DB 8;
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                                                                                                                                                                                                                                                                                     DB
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RESULT 1324
ID AAQ6721
DE Human c
PN CA21116
                                 Best Loca
RESULT 1332
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RESULT 1329
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RESULT 1326
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AAX86357 standard;
Rat smooth muscle :
WO9936101-A1.
                                                                                                                                                                                                                                                       Human sidekick homologue WO2004076622-A2.
                                                                                               AAK69400 standard; DNA; 11456 Bp.
Human immune/haematopoietic antigen
                                                                                                                                                                           Sorangium cellulosum tmbA
US2003054547-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cervical cancer marker WO200142467-A2.
                                                                                                                                                                                     ADC26983 standard; DNA; 11358 BP.
Sorangium cellulosum tmbA gene cluster tmbC DNA
                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

2.3%; Score 34.2; DB 4;

It Local Similarity 53.3%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADT48680 standard; cDNA;
Bacterial polynucleotide
US2003233675-A1.
                                                                                      WO200157182-A2.
                                                                                                                                                                 20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide encoding cDNA WO2004041170-A2.
                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                             ADP25090 standard; cDNA; 3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellobiohydrolase
WO9906574-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ67210 standard; DNA; 1423
Human corticosteroid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KONN ) GIST-BROCADES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX22095 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HINK/) HINKLE G
(SLAT/) SLATER S
                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7:-JUN-1994
                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                      NAT INST ADVANCED IND SCI & TECHNOLOGY.

th 2.3%; Score 34.2; DB 13;

Similarity 56.8%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ALLELIX BIOPHARMACEUTICALS ch 2.3%; Score 1 Similarity 47.6%; Pred.
                                                                                                                                                      JULIEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                 GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOLDMAN B S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHEN X
                                                                 GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4
          myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DNA; 1767 BI
CBH B coding
                                         2.3%;
                                                                                                                                                                                                                                                                                                           2.3%;
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2.3%;
54.3%;
                                                                                                                               2.3%;
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                                                                SCI INC.
                                                                                                                                                                                                                                                                                        6999
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                                                                                                                                                                                    gene
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                                          Score
Pred.
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Pred.
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Pred.
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Pred.
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globulin
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Pred.
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          chain
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No. 2.
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No. 4.
                                          No.
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No. 1
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34.2;
No. 1.
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No.
                                                                                              genomic
                                                                                                                                                                                                                                                                                                                                                                 NO:2268.
          gene
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                                          . 2;
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                                                                                                                               DB 10;
.1e+02;
                                          DB 4;
.1e+02;
                                                                                                                                                                                                                                                                                                           DB 13;
.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
.4e+02;
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.6e+02;
                                                                                                                                                                                                                                                                             of.
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                                                                                                IJ
                                                                                                NO:24212.
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Best Local Similarity
RESULT 1339
ID AAF88314 standard; D:
DE S. spinosa DNA fragm
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB ) BAYER AG.
                                                        Best Local Similarity
RESULT 1340
ID AAP88317 standard; D
DE S. spinosa DNA fragm
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB ) BAYER AG.
                            RESULT
                                                                                                                                                                                                                                                                 вевt Local Similarity
RESULT 1338
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ID AI
DE SC
PN US
PD 20
  BBU
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                                                                           AAF88317 standard; DNA; 29736 BP.
S. spinosa DNA fragment SEQ ID 6.
DE19957268-A1.
                                                                                                                                              AAF88314 standard; DNA; 25360 BP.
S. spinosa DNA fragment SEQ ID 3.
DE19557268-A1.
08-MAR-2001.
                                                                                                                                                                                                                                                                                                          Cephalosporin antibiotic
JP02291274-A.
03-DEC-1000
AAD56078 standard; DNA; Mouse Map3k6 carcinoma; WO2003035837-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-2002.
(OWEN/) OWENS G K.
(MANA/) MANABE I.
                                                                                                                                                                                                                                     Human genomic se
WO2003073826-A2.
                                                                                                                                                                                                                                              ACN44414 standard; DNA; 24492 BP.
Human genomic sequence hCG1780827
                                                                                                                                                                                                                                                                                                                                                                                               Sorangium cellulosum tmbA gene cluster US2003054547-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADC26981 standard; DNA; 20922 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human periodontal
WO2004042054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003017549-A1.
23-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA60861 standard;
Rat smooth muscle :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200259270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN84504 standard; DNA; 16011 BP.
Rat smooth muscle myosin heavy chain gene (-4216
                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUBI-) HUBIT GENOMIX INC. (KAMO/) KAMOI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN37218 standard; DNA; 20001
                                                                                                                                                                                                                   SAGR-)
                                                                                                                                                                                                                                                                                                                                                                            JULI/) JULIEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OWEN/) OWENS G K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                     ocal Similarity
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                                                                                                                                                                                             SAGRES DISCOVERY.
h 2.3%;
Similarity 60.0%;
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h 2.3%;
Similarity 45.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myosin heavy chain
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                                     2.3%;
47.8%;
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47.8%;
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         ; 32069 BP.
associated
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No. 5.
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No.
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No.
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No. 4.
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No. 4.
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No. 5.9e+02;
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No.
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No. 4.
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No. 5.
                                     5. 6.
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        gene
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.8e+02;
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.5e+02;
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.4e+02;
                                     DB 4;
.5e+02;
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.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
.8e+02;
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.8e+02;
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                                               29736;
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Best Local Similarity RESULT 1350
                                                                                                                                     Best Local Similarity
RESULT 1349
                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1348
                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1347
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RESULT 1346
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Best Local Similarity
RESULT 1342
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MOUBE MAD346 CARCAMO
MO2003057146-A2.
) 17-JUL-2003.
A (SAGR-) SAGRES DISCOVERY.
2.3%; SAGRES DISCOVERY.
46.4%;
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence o
US6280999-B1.
28-AUG-2001.
                                                                                                   Human ribosomal US2002160970-A1.
                                                                                                                                              (SAGR-) SAGRES DISCOVERY.

"XY Match 2.3%;

It Local Similarity 48.7%;
                                                                                                                                                                                          ACN45116 standard; DNA; 42772 BP. Mouse genomic sequence mCG8527. wo2003073826-A2.
                                                                                                                                                                                                                                                                           ADA37416 standard; DNA; 41907
Human rDNA repeat unit.
US2003108914-A1.
12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS12439 standard; DNA; 37590 BP. DNA encoding 1-aminocyclopropane WO200168879-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB72179 standard; DNA; 32069 Mouse Map3k6 gene. WO2003008583-A2.
Invertebrate foraging WO200259370-A2.
                     ABS65032 standard; DNA;
                                                                (HADL/) HADLACZKY G. (SZAL/) SZALAY A A.
                                                                                                                          ADA14747 standard;
                                                                                                                                                                                                                                                                                                                                                                               WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                          ADQ97084 standard; DNA; 38690 BP.
Human cancer associated sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KOSA-) KOSAN BIOSCIENCE.
ry Match 2.3%;
t Local Similarity 56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS17367 standard; DNA; 33529
DNA sequence of S. cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY.
ry Match 2.3%;
t Local Similarity 46.4%;
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                                                                                                                                                                                   L2-SEP-2003
                                                                                                                                                                                                                                                               (HADL/) HADLACZKY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
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th 2.3%;
Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                  SAGRES DISCOVERY INC.
h 2.3%;
Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ndard; DNA; 32069 BP. carcinoma associated
                                                                                                               DNA
                                                                                                              DNA; 42998
A complete 1
                                                                                                                                                                                                                                         2.3%;
                                            2.3%;
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         A; 42999 BP.
behaviour a
                                            Score
Pred.
                                                                                                             8 BP.
repeating
                                                                                                                                                                                                                                                                                                                                  Score
Pred.
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Pred.
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Pred. No. 7.8e+02;
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polyketide
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          associated
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No.
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No.
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No. 6.
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No. 6.
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No. 6.8e+02;
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                                                                                                                                                                                                                                         DB 9;
.8e+02;
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.5e+02;
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.8e+02;
                                            DB 8;
.9e+02;
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.4e+02;
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.9e+02;
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.8e+02;
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          human
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         DNA sequence
                                                     Length
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01-AUG-2002

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ID DE PA PA PA PA PA
                                                                            Best Local Similarity
RESULT 1358
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Best Local Similarity
RESULT 1355
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RESULT 1353
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                                                                                                                                                                                                                    Query Match
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                                                      ADA03083 standard; DNA; 93483 Mouse mCG17918 carcinoma assoc
                                                                                                                                                     Genomic DNA encoding US2002132291-A1.
                                            WO2003057146-A2.
                                                                                                         (KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
                                                                                                                                                                                                                                                   Mouse cancer-associated WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                    ADC26995 standard; DNA; 67251 BP. Sorangium cellulosum tmbA gene cluster. US2003054547-A1.
                                                                                                                                                                                   ABX14763 standard; DNA; 88191 BP
                                                                                                                                                                                                                                                                       ABD32576 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP84151 standard;
Human CA125 genomic
WO2004045553-A2.
                                                                                                                                                                                                     (SAGR-) SAGRES DISCOVERY INC.
ry Match
Local Similarity 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ribosomal DNA complete repeating US2004163147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD61411 standard; DNA; 42999 BP. Human ribosomal DNA (rDNA) repeat US2003101480-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ97534 standard; DNA;
                                                                                                                                                                                                                                                                                                                           0-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                              (SAGR-) SAGRES DISCOVERY INC.
cy Match 2.3%;
Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR43949 standard; DNA; 42999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HADL/) HADLACZKY G. (SZAL/) SZALAY A A.
                                                                                                                                                                                                                                                                                                                 JULI/) JULIEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HADL/) HADLACZKY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEUR-) NEUROSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
  ocal Similarity
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                        Match
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                       SAGRES
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3 DISCOVERY.
2.3%;
arity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                    2.3%;
51.7%;
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2.3%;
47.4%;
                                                                                                                                                                         novel human
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amino
                                                                                                                                                                                                                                                           80423 BP.
genomic DNA MD7-205.
                                                                                                                                                                                                                                                                                                                                                                                                                                  58687 BP.
sequence MD09-010,
                                                      associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S FOUND INC.
3%; Score 34.2;
4%; Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat region.
                                                                                   Score
Pred.
  Score 34.2; DB 9;
Pred. No. 1.1e+03;
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Pred.
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Pred.
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No.
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No. 1.
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No. 9.
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No. 9.
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No.
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No. 7
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No. 7
                                                     gene,
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7. 1.
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                                                                                                                                                                                                        DB 13;
.1e+03;
                                                                                                                                                                                                                                                                                           DB 10;
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
).1e+02;
                                                                                    DB 8;
.1e+03;
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.9e+02;
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.9e+02;
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.9e+02;
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                                                     NO:1601
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           93483;
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                                                                                                                                                                                                                                                                                                    67251;
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Best Local Similarity
RESULT 1368
ID ADP75180 standard; D:
DE Human Endophilin 2 g
PN W02003031594-A2.
PD 17-ABR-2003.
PA (GENO-) GENOME THERA
                                                                                                                                              Best Local Similarity RESULT 1367
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Best Local Similarity
RESULT 1365
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                                                                                                                                                                                        Mouse cancer-associated WC2004074320-A2.
                                                                                                                                                                                                                                                      ADL13512 standard; DNA; 178870 BP.
Osteoarthritis-associated polymorphic nucleotide
WO2003054165-A2.
03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
2.3%; Score 34.2; DB 10;
                                                                                                           ADF51132 standard; DNA; 243428 BP. Human P-Rex1 genomic DNA sequence. W02003080664-A1.
                                                                                                                                                                                                                                                                                                                                                                              ABN95044 standard;
Gene #1542 used to
WO200229103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine cancer-associated (CA) g W02004058146-A2.
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(MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
                                                                                      (BABR-) BABRAHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse genomic se
US2003216558-A1.
                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC
                                                                                                                                                                                                                                                                                                                                                                       11-APR-2002
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PROPERTY MATCH 2.3%;
It Local Similarity 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA66367 standard; DNA; 93483
Mouse mcG17918 gene genomic DN
WO2003053224-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence for
                                DNA;
                                                                                                                                                                                                                                                                                                                                 INC.
2.3%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                       DNA; 110096 BP. diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%;
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53.3%;
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i genomic
                                            304905
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for mCG17918.
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Pred.
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No. 1.
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No. 1.
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No. 1.
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No.
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No. 1.
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No. 1.
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No. 1.1e+03;
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                                                                DB 12;
.8e+03;
                                                                                                                                                       DB 13;
.7e+03;
                                                                                                                                                                                                                                             DB 10;
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..le+03;
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.2e+03;
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.2e+03;
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.2e+03;
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.1e+03;
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                                                                                                                                                                                                                                                                                                                                             110096;
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THERAPEUTICS

CORP

16-OCT-2003

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Best Local Similarity RESULT 1375
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                          Best Local Similarity RESULT 1376
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RESULT 1369
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                                                                                                                  Query Match
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(KANS-) KANSAI TECHNOLOGY LICENSING 2.3%; Score 3.5 Match 2.3%; Pred. 1
ACH73361 standard;
Human genome derive
US2003194704-A1.
                                                                             cDNA sequence #607
                                                                                         ABK36216 standard;
                                                                                                                                            US6551795-B1.
                                                                                                                                                   Pseudomonas aeruginosa polynucleotide
                                                                                                                                                              ABD16714 standard; DNA; 429 BP
                                                                                                                                                                                                           07-SEP-2001
                                                                                                                                                                                                                   AAI84784 standard; cDNA; 400 BP.
Human polynucleotide SEQ ID NO 4
WO200164835-A2.
                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                    DNA encoding novel
                                                                                                                                                                                                                                                                                                              AAS69541 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice isoprenoid
US2004010815-A1.
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Kidney disease-associated gene-related
WO2003091427-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-1995.
(NITA-) JAPAN TAFU
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Exon 4 of rice pyro
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                                                              8-OCT-2001
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GHASSEMIAN M.
BRIGGS S P.
COOPER B.
                                                     GENETICS
                                                                                                                          GENOME THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                    KREPS J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA
rice pyruvate
        ndard; DNA; 510
derived single
                                  inst inc.
2.3%;
ty 52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis-associated
                                                                                                                                                                                                                                                                                                    cDNA;
                                                                              encoding novel human
                                                                                         cDNA; 455 BP
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                                                                                                         2.3%;
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47.6%;
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60.5%;
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                                                                                                                                                                                                                                                                                                   390 BP.
diagnostic
        BP.
exon
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                                    Score
Pred.
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Pred.
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        probe
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34;
No. 7
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No. 2e+03;
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No.
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No.
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87;
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93;
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90;
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67;
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         #6556
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                                                                              secreted protein.
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Best Local
RESULT 1384
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RESULT 1383
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RESULT 1382
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RESULT 1379
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RESULT 1378
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                                       AAK52313 standard; cl
Human polynucleotide
WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PENN/)
(RANK/)
(HANZ/)
                                                                                                                     Pseudomonas aeruginosa
US6551795-B1.
                                                                                                                                                                                                     ABD16865 standard; DNA; 1383 BP. Pseudomonas aeruginosa polynucleotide US6551795-B1.
                                                                                                                                ABD16805 standard; DNA; 1503 BP.
Pseudomonas aeruginosa polynucleotide
                                                                                                                                                              (GENO-) GENOME THERAPEUTICS ry Match 2.3%; t Local Similarity 49.4%;
                                                                                                                                                                                                                                                                            WO200175067-A2.
11-OCT-2001.
                                                                                                                                                                                                                                                                                               DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV06518 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa polynucleotide US6551795-B1.
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(GEHO ) GEN HOSPITAL
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Rat gene AA799755,
WO2003016475-A2.
                       (HYSE-)
                                                                                                                                                                                             22-APR-2003
                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                          AAS90702 standard;
                                                                                                                                                                                                                                                                                                                                                                      WO2004070035-A2.
                                                                                                                                                                                                                                                                                                                                                                               ADR46465 standard; DNA; 895 BP.
Tobacco caltractin-like protein coding
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(FARB ) BAYER AG.
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) RANK D R.
) HANZEL D K.
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 Similarity
                    HYSEQ INC.
                                                 cDNA;
de SEQ
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SEQ ID
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human diagnostic
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2.3%; Score 34;
46.6%; Pred. No.
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2.3%;
57.5%;
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ID NO 858.
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NO 11114.
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1.7e+02;
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1.6e+02;
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1.2e+02;
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                                                                                                                                                                                                                                               DB 5;
1.5e+02;
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1.3e+02;
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1e+02;
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1.2e+02;
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ABX05202 standard; cDNA; 2154 BP.

#217

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Query Match
Best Local Similarity
RESULT 1393
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Best Local Similarity
RESULT 1391
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RESULT 1388
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RESULT 1387
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RESULT 1386
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                    Human reproductive WO200155320-A2.
                                        AAL04774 standard;
                                                          (SYCN) SYNGENTA PARTICIPATIONS AG.
ry Match 2.3%; Score
t Local Similarity 61.1%; Pred.
                                                                                                        WO2004061080-A2.
                                                                                                                 Rice stress-related
                                                                                                                                                                               ADQ36980 standard; DNA; 2844 BP. Cell proliferation-related nucleic WO2004061122-A2.
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                                                                                                                            ADQ15650 standard;
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(SYCN) SYNGENTA PARTICIPATIONS AG.
2.3%; Score
t Local Similarity 61.1%; Pred.
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(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                             Human cDNA of the invention EP1347046-A1.
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Human tumour-associated a
WO2004060270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA53499 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour-associated a WO2004060270-A2.
22-UUL-2004.
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(HYSE-) HYSEQ INC.
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h 2.3%; Score
Similarity 57.5%; Pred.
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C BIOTECHNOLOGY.
2.3%; Score ?
                           DNA; 3051 BP.
system related antigen DNA
                                                                                                              DNA; 2844
d protein c
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invention SEQ ID
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SEQ ID 1067.
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antigenic
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lantigenic
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2.3e+02;
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2.3e+02;
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2.1e+02;
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2.1e+02;
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2e+02;
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standard;

DNA; 12342

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Best Local Similarity RESULT 1402 ID ACC48895 standard;
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Best Local Similarity
RESULT 1401
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Best Local Similarity
RESULT 1398
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RESULT 1396
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(INSP ) INST PASTEUR.
(INSP ) INST FRANCAIS DU PETROLE.
(INSF ) Atch 2.3%; Score
2.3%; Pred.
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Best Local (
                                                         ABL15220 standard; cDNA; 10479 Bp. Drosophila melanogaster expressed W0200171042-A2.
                                                                                                                                                            ACC48896 standard; DNA; 870 Rhodococcus ruber eth gene
                                                                                                                                                                                                                                       AAQ98237 standard; DNA; 8626 BP. Partial rice pyruvate orthophosphate dikinase JP07184657-A. 25-JUL-1995.
                                                                                                                                                                                                     (NITA-) JAPAN TAFU GURASU KK.
"ITY Match 2.3%;
It Local Similarity 61.1%;
                                                                                                                                                                                                                                                                                                                                    Human proton/oligonucleotide transporter WO200160854-A1.
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ry Match 2.3%;
t Local Similarity 52.9%;
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30-MAY-2002.
(DIAD-) DIADEXUS INC.
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h 2.3%;
Similarity 52.9%;
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Pred. No.
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No.
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4.4e+02;
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4.1e+02;
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4e+02;
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2.7e+02;
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2.7e+02;
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2.7e+02;
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2.8e+02;
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2.7e+02;
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2.4e+02;
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RESULT 1403
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                                         ACC48894 standard;
Rhodococcus ruber e
EP1270722-A1.
                                                                                                                              Mouse pre rRNA 9
US2004163147-A1.
                                                                                                                                                                                                                  ACC44629 standard; DNA; 22118 BP. Mouse ribosomal RNA gene (rDNA) nucleotide WO200297059-A2.
                                                                                                                                                                                                                                                                                             ADF10518 standard; DNA; 22118 Mouse ribosomal RNA gene repea WO2003093469-A2.
13-NOV-2003.
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(HADL/) HADLACZKY G.
(SZAL/) SZALAY A A.
            (INSP )
                                                                                                                                                   ADR43948 standard; DNA; 22118
                                                                                                                                                                      JS-DEC-2002.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

2.3%; Score 34;
rv Match

56.0%; Pred. No.
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Mouse ribosomal DNA (rDNA) repeat region.
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US2003108914-A1.
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Origin of replication DNA.
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US2002160970-A1.
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WO200259265-A2.
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(SZAL/) SZALAY A A.
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ry Match 2.3%;
Local Similarity 63.4%;
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2.3%; Scor
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6.4e+02;
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RESULT 1415
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Genomic DNA #38 encoding human colc
US2002119919-A1.
29-AUG-2002.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
Human immune/haematopoietic antigono200157182-A2.
                                                 (HUMA-) HUMAN GENOME SCI INC.
Pry Match 2.3%;
St Local Similarity 57.5%;
                                                                                   ADB92987 standard; DNA; 25424 BP.
Human colorectal cancer related polypeptide
US2003054420-A1.
20-MAR-2003.
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02-AUG-2001.
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Human colorectal cancer related polypeptide DNA
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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       Mouse Gnb1 gene.
WO2003008583-A2.
                          ADB72467 standard;
                                            (SAGR-) SAGRES DISCOVERY.
ry Match 2.3%;
t Local Similarity 54.9%;
                                                                                       Human GNB1 gene. WO2003008583-A2.
                                                                                                           ADB72470 standard; DNA; 50396
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Human GNB1 carcinoma
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                                                                               30-JAN-2003
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Human liver glucokinase genomic DNA.
WO200224741-A2.
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                                                                                                                                                                                                                                                                                                                     (RYAN/) RYAN J W.
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02-AUG-2001.
(HUMA) HUMAN GENOME SCI INC.
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Human immune/haematopoietic antigen
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ma associated gene,
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9.7e+02;
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9.2e+02;
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9e+02;
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9.7e+02;
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Query Match
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RESULT 1437
ID ADE95749 i
DE Mouse Bacl
PN W02003039
PD 15-MAY-200
PA (SAGR-) SJ
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RESULT
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RESULT 1431
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RESULT 1429
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                   ADE95749 standard; DNA; 96597 Mouse Bach2 gene genomic DNA; WO2003039484-A2.
                                                                                                         Mouse Bach2 gene. WO2003008583-A2.
                                                                                              30-JAN-2003
                                                                                                                            ADB72239 standard; DNA; 96597
                                                                                                                                                                                                                                                                                ADQ17634 standard; DNA; 96276 BP. Human soft tissue sarcoma-upregulated WO2004048938-A2.
                                                                                      (SAGR-)
                                                                                                                                                                                              WO2003057146-A2.
                                                                                                                                                                                                           Mouse Bach2
                                                                                                                                                                                                                  ADA02501 standard;
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Sorangium cellulosum disorazole polyketide synthase
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15-MAY-2003.

(SAGR-) SAGRES DISCOVERY.

21Y Match 2.3%;

21Y Match 54.9%;
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WO2003039484-A2.
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Human GNB1 gene genomic DNA sequence.
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th 2.3%;
Similarity 50.0%;
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1.3e+03;
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1.3e+03;
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1.3e+03;
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1.2e+03;
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9.7e+02;
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RESULT 1451
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RESULT 1450
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RESULT 1446
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RESULT 1443
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RESULT 1444
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03-JUL-2003.
03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
2.3%;
ery Match
2.3%;
57.5%;
                                             ADL13501 standard; DNA; 167932 BP.
Osteoarthritis-associated polymorphic
                                                                                                               ADQ59449 standard; DNA; Human cancer-associated WO2004058288-A1.
                                                                                                                                                                                      ABZ35015 standard; cDNA; 136328 BP. Human gene expression profile polynucleotide WO200274979-A2.
                                        WO2003054166-A2.
                                                                                                                                                                                                                         (UYEC-) UNIV EAST CAROLINA.

ry Match 2.3%;
t Local Similarity 34.7%;
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Human adenosine Al receptor antisense
                                                                                                                                                                                                                                                                                                                              02-SEP-2004
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                                                                                                                                                                                                                                                                                                                                               Mouse cancer-associated genomic
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ry Match 2.3%;
Local Similarity 47.2%;
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1.6e+03;
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RESULT 1460
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RESULT 1457
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RESULT 1454
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Human bone marrow WO200157276-A2. 09-AUG-2001.
                                                                                                                                                                                                                                                   Pseudomonas aeruginosa polynucleotide
US6551795-B1.
22-APR-2003.
                                                                                            Probe #7553 used to WO200157272-A2.
                                                                                                                                                                            ABA59121 standard; DNA; 454 BP. Human foetal liver single exon W0200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer associated sequence HD08-007, WC2004060304-A2.
                                 AAK33067 standard; DNA; 454
                                                                                                                  AAI38867 standard;
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Bovine EST associated with lactation/muscle/fat
US2002137139-A1.
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18-OCT-2001.
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ry Match 2.3%;
t Local Similarity 48.7%;
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29-MAY-2003.
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(FISH/) FISHER D K.
(LIUJ/) LIU J.
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                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS
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(MATH/) MATHIALAGAN
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synthase EST #225.
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o measure
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No. 97;
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No. 1e+02;
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No.
                    exon probe SEQ ID NO:
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1e+
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5. 1e+02;
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1.
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2.3e+03;
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                                                                                                                                      DB 4;
.1e+02;
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Best Local Similarity RESULT 1462
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RESULT 1465
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                                                                                                                                                         Best Local Similarity RESULT 1469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE PA
RESULT
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Best Local Similarity
RESULT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                    Query Match
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DRMA/) DRMANAC R T.
(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon probe WO200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynuclectide SEQ ID N WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver sin WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon
                                                                                                                                                                                                                                                                Human ovarian cancer WO200170979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD16019 standard; cDNA; 517 cDNA (SeqID 87) that confers WC2003020741-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACH15828 standard; cDNA; 473
Human adult heart cDNA #142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK07302 standard; DNA; 454 BP.
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                                                                                             Human cDNA clone EP1074617-A2.
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27-SEP-2001.
(MILL-) MILLENNIUM PREDICTIVE
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TY Match 2.3%; Score
Local Similarity 50.3%; Pred.
                                                         (HELI-) HELIX RES INST
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y Match 2.3%; Score
Local Similarity 50.3%; Pred.
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                 ocal Similarity
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2.3%; Sc
Ly 50.3%; Pr
                                                                                                                 1; cDNA; 572 (3'-primer)
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                                                                                                                                                                                                                                                                                 DNA; 531 BP.
er DNA marker #18996.
                                                                                                                                                                                                                                                                                                                                             2.3%;
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46.0%;
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NO 8685.
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Pred.
                   Score 33.8;
Pred. No. 1
                                                                                                                                                                                 MEDICINE INC.
Score 33.8; DB 5;
Pred. No. 1.1e+02;
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No. 1.1e+02;
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No. 1.
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No. 1.1e+02;
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.1e+02;
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.le+02;
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.1e+02;
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.1e+02;
                     DB 4;
.2e+02;
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.le+02;
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Query Match
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RESULT 1476
ID AADOCCO
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RESULT 1474
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RESULT 1475
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RESULT 1473
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Best Local Similarity RESULT 1477
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                Query Match
                                                                                                         Human gene fra JP10057062-A. 03-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence WO200255712-A2. 18-JUL-2002.
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                                                                                                                                                                            AAC38557 standard; DN
Arabidopsis thaliana
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK89970 standard;
                                                   AAH03867 standard; cDNA; 765
Human cDNA clone (5'-primer)
                                                                                                                                   AAV15437 standard;
                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                             22-ARR-2003.
(GENO-) GENOME THERAPEUTICS
2.3%;
ry Match 2.3%;
46.4%;
                                                                                                                                                                                                                                                  Pseudomonas aeruginosa polynucleotide
US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002059663-A1.
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Arabidopsis thaliana po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER AG.
                                   EP1074617-A2.
07-FEB-2001.
                                                                                                                                                                                                                                                                    ABD17092 standard;
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                          (HELI-) HELIX RES INST.
                                                                             (RIKA ) RIKAGAKU KENKYUSHO.
2.3%;
ry Match 2.3%;
t Local Similarity 50.3%;
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PRICE J L.
RAINES T M.
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WDESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
ALLEN K.
HOFFMAN N.
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tag (EST)
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          Score 33.8; DB 4;
Pred. No. 1.4e+02;
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No.
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.1.3e+02;
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.2e+02;
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.2e+02;
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.3e+02;
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.3e+02;
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.4e+02;
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Query Match
Best Local S
RESULT 1480
  ADO03013 standard; cDNA; 820 BP.
Corn orthologue of Thalecress transcription factor, cDNA #124.
US2004045049-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC44956 standard; DNA; 774 BP.
Arabidopsis thaliana DNA fragment SEQ ID NO:
EP1033405-A2.
                                                                                                                                                                                                                                                                              ADI42806 standard; DNA; 820 BP.
Plant transcription factor polynucleotide #811.
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                             (YUGG,
                                                                                                                                                                                                                                                                         JS2004019927-A1.
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                                            (REUB,
                                                                  ADAM,
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1480
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RIECHMANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILIGRIM M L.
DUBELL A N.
PINEDA O.
                                                        ZHANG J.

FROMM M E.

HEARD J E.

RIECHMANN J J.

ADAM L J.

BROUN P E.
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
JIANG C.
SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
                                   PINEDA O.
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PRICE J L.
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YU Y.
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RESULT 1487
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RESULT 1485
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                                                                                                                                                   Rice gene, SEQ I. WO2003000898-A1.
                                                                                                                                                                                                                                  ADK66947 standard; DNA; 882
Gene #37 for inhibitory RNA
WC2003068961-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUBE/)
(RATC/)
(KUMI/)
(SHER/)
                                                                     Human steroid-induced US6673549-B1.
                                                                                                                                                                                                                                                                                                                 ABZ81831 standard; DNA; 882 FRP nucleic acid sequence. WC2003012082-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 AAD52559 standard; DNA; 882
SARP 1 DNA.
WO200290992-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding secreted WO200277204-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AVET) AVENTIS PHARMA SA.
2.3%;
It Local Similarity 49.2%;
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AAV60339 standard; cDNA; 1120 BP.
cDNA sequence of fibroblast growth factor-2 (FGF-2)
                                                             06-JAN-2004
                                                                               ADL12563 standard; cDNA; 1004 BP.
Human steroid-induced C3A liver c
                                                                                                                                           03-JAN-2003
                                                                                                                                                                       ADA69490 standard;
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                                                   (INCY-)
                                                                                                                                                                                                               (AXOR-) AXORDIA LTD.
                                                                                                                                                                                                                                                                                              (AXOR-) AXORDIA LTD.
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th 2.3%; Score
Similarity 53.4%; Pred.
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G961 orthologous
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1.4e+02;
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.6e+02;
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.5e+02;
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.5e+02;
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Best Local Similarity
RESULT 1492
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Best Local Similarity
RESULT 1496
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Best Local Similarity
RESULT 1495
                          Best Local Similarity RESULT 1498
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RESULT 1497
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Best Local S
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                                                                                                                                                                                                                                                                                   AAH13860 standard; cDNA; 1809 BP.
Human cDNA sequence SEQ ID NO:10847.
EP1074617-A2.
07-PEB-2001.
(HELI ) HELIX RES INST.
Query Match
2.3%; Score 33.
Best Local Similarity 52.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9837880-A1.
03-SEP-1998.
(CIBL-) CIBLEX
                                                                                                                                                                                                         Human disease related protein DNA sequence SeqID246. WO2003018621-A2. 06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 1569 BP.
DNA encoding human alanine aminotransferase
WO200255712-A2.
18-JHI--7000
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29-APR-2004.

(FIVE-) FIVE PRIME THERAPEUTICS INC.
2.3%; Score 33.8;
2.5% Score 33.8;
2.5% Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP28745 standard; DNA; 1344 BP. Human secreted protein encoding WC2004035732-A2.
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Human secreted protein encoding sequence
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Full length cDNA for
US6306613-B1.
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(CIBL-) CIBLEX CORP
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                                                                                                            ADR25867 standard; DNA; 1809 BP.
Breast cancer prognosis marker #1728.
WO2004065545-A2.
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ADA70200 standard; DNA; 1980 BP.
Rice gene, SEQ ID 3523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIBL-) CIBLEX CORP.
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Ty Match 2.3%; Score 33.8;

Local Similarity 50.3%; Pred. No. 1.
                                         (ROSE-) ROSETTA INPHARMATICS LLC.
(NECA-) NETHERLANDS CANCER INST.
TY MATCH 23%; SCOTY
Local Similarity 52.5%; Pred
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h 2.3%; Score 33.
Similarity 52.5%; Pred. No.
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Pred. No. 1.
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Pred. No. 1.7e+02;
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Pred.
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Pred. No. 2.1e+02;
                                            Score 33.8; DB 13; Pred. No. 2.1e+02;
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.7e+02;
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.7e+02;
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.8e+02;
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.1e+02;
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Best Local Similarity
RESULT 1500
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Best Local Similarity
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03-JAN-2003.
(SYGN ) SYNGENTA
                                     Gene sequence #SEQ ID 2646.
EP1258494-A1.
20-NOV-2000
                                                                                                                                               ADA48189 standard; DNA; 1980 BP.
Rice gene conferring disease resistance
WO2003000906-A2.
                                                                                                                                       03-JAN-2003
                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG-
ry Match 2.3%; Score
t Local Similarity 54.4%; Pred.
                        (CELL-)
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h 2.3%; Score 33.8;
Similarity 54.4%; Pred. No. 2
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Run

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Result
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Goddwski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (brit; S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primar for synthesizing full-length cDNA and use thereof Petent: JP 2002191363-A 14510 09-UUL-2002;
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                                       CACTCTGAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTTCCTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0;
0; Mismatches
                                 Location/Qualifiers
                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Location/Qualifiers (100). .(
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Query Match 98.5%; Score 1462.4; DB 6; Length 3375; Best Local Similarity 99.9%; Pred. No. 0; Matches 1463; Conservative 0; Mismatches 1; Indels 0; Gaps	Qy         7 ACACGCAGCTAGCCGGAGCCCGGACCAGGCGCTTGTGCCTCCTCCTCGTCGCCGCG 66	Qy         67         TCCGCGAAGCCTGGAGCCGGGGAGCCCCGCGCTCGCCATGTCGGGGGAGCTCAGCAAC         126           Db         61         TCCGCGAAGCCTGGAGCGGGGGGGGGGGGGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCAAC         120	Qy         127 AGGTTCCAAGGAAAGGCGTTCGCTTGCTCAAAGCCCGCAGGAGGCTCGCC 186	Qy         187 GAGATCAACCGGGAGTTTCTGTGACCAGAAGTACATGAAGAACCTTCCAGAA 246	Qy         247 AAGCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATT 306	Oy 307 GACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCTGGAG 366	Oy 367 AIGAAGAAGAIGAICCAGAGGIGACAGGGGICAGIGACACTAIAICCTACCGAGAC 426	Oy 427 TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATTTGAA 486	Qy         487 GGAAAAGCCAACGAGGCCCCAAGCCAAGTCGCCCCCTCCAGAGAGACATTGCT 546	Qy         547 AGCCTGCCCTGAGGACCCCGCCTGGACTCCCCCAGCCTTCCCATACCTCCCTC	Oy 607 ATCTTGCTCCCTTCTTGACACACTGTGATCTCTCTCTCTC	Qy 667 GGGTTTGTTTTGTTTTGATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGG 726	Qy 727 CTCTGGGAAATCCTGAGCCTTGGGTCCCTCCTTCTTCTTCCTTC	Qy         787 CTCCCTGTGCAGAAGGCCTGATATCAAACCAAAAACTAGAGGGCAGGGCCAGGGCCAGG         846           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	847 GAGGCTTCCAGCTGTTTCCCCTCACTTGAAGGAACCAGCACTCCCTTTCAGAA	907 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCT	Db 901 AGTCTCCAAGCCTCACGCTCACTGACTCGAGGCCTCTGAGGAGACCCCAGGCCACTT 960 Qy 967 GAGAAGACCTTGGAGTAGGGAAGGCTGCAAGGCCTCTTTCGGGTTTTCCTTGGACAGTG 102	Db 961 GAGAAGACCTTGGAGTAGGGACAGAGGCTCTTTTCGGGTTTCCTTTGGACAGTG 102
907 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCT 966	967 GAGAAGACCTTGGAGTAGGGACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTG 1026 	1027 CCATGGTTCCAGTGTCTCACCCAGGACACACCACTCGGGGCCCCGCTGCCCCA 1086	1087 GCTGATCCCCACTCATTCCACACCTCTTCTCATCCTCAGTGATGTGAAGGTGGGAAGGAA	1147 AGGAGCTTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGGTC 1206	1207 TCTGGCCACACCTGTGCAGGCAGCTGAGGCAGCGTGCAGCCCTACTGCTCGTTACTGG 1266	1267 GGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTTGGGGGGAAAGGTCAGCTC 1326 	1327 AGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGACCAGGATGGGAGAATGAGGAGTA 1386	1387 AAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGACTGAGAATACAAGGTTGCT 1446 	1447   TGTCTGACCCGARCTGGTTGAA   1470 		LOCUS AX882339 3375 bp DNA linear PAT 17-DEC-2003 DEFINITION Sequence 17244 from Patent EP1074617. ACCESSION AX882339 VERSION AX882339.1 GI:40037187	KEYWORDS . SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.	TITLE Primers for synthesising full-length cDNA and their use JOURNAL Patent: EP 1074617-A 17244 07-FEB-2001; Research Association for Biotechnology (JP)	FEATURES LOCATION/QUALILLE'S  13375  / organism="Homo sapiens"  / mol_type="unassigned DNA"	CDS 100 . 552 /note="unmamed protein product" /codon start=1	protein_id="CAE91540.1" db_xref="G1:40037188" translation="MSGELSNRFQGGKAFGLLKARQERRLABINRELL	нα

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Isogai, T. and Otsuki, T.

Burect Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- £ 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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LPEKLTAFKEKYMEFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDT
ISYRDFVNMMLGKRSAVLKLVMMFEGKANESSPKPVGPPPERDIASLP"
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      Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
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1..337
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/cell_type="texatocarcinoma"
/clone_lib="NT2"
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/proteIn_id="BAB14269.1"
/db_xref="G1:10434475"
                                                                                                Genet. 36 (1), 40-45 (2004)
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Matches 1463; Conservative
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                                                                     human cDNAs
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                                    CCATGGTTCCAGTGCTCTGGTGTCACCCAGGACACACACTCGGGGCCCCGCTGCCCCA 1080
                                                                                                                                                            TCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAGCGTGCAGCCCTACTGTCCCTTACTGG 1260
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                                                                                                                                                                                                                                                                                              1141 AGGAGCTTGGCATTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 1200
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                TCTGGCCACCTGTGCAGGCAGCTGAGAGGCAGCGTGCAGCCCTACTGTCCCTTACTGG
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AK022845.1 GI:10434474
Oligo capping; fis (full insert sequence).
Momo sapiens (human)
Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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		SOURCE UNKNOWN.   SORGANISM UNKNOWN.   ORGANISM UNKNOWN.   Unclassif   REFERENCE 1 (bases   AUTHORS Hillman, J   666   TITLE Human imm   G60   JOURNAL Patent: lm	726 PEATURES 720 ORIGIN 786 Query Matc	Matches 1459; Constructive   Matches 1459; Constructive   Matches 1459; Constructive   Matches 1459; Constructive   Mismatch   Mis	CAGAA         906	ACTCT 966  Qy 127 AGGTTCCAAGGAGGAAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGGAGGCTGGCC ACTCT 960  Db 120 AGGTTCCAAGGAGGAAGGCGTTCGCTTGCTCAAAGCCCGGCAAGGAGGAGGAGCTTGCTCAAAGCCCGGCAAGGAGGAGGAGGCTTGCTCAAAGCCCGGCAAGGAGGAGGAGGCGCTGCTCCAAAGCCCCGGCAAGGAGGAGGAGCGCTGCTCCAAAGCCCCGGCAAGGAGGAGGAGCGCCGCCCAAAGCCCCAAAAGCCCCAAAAGCCCCAAAAGCCCCAAAAAA	CAGTG 1020 Db	1080  24) AGCTCACAGCCTTCAAAGAAGAAGAACTACAGAGTTTGACTGAACAACTACAGAGTTTTGACTGAACAACTACAGAGATTTTGACTGAACAATGAAGGGGAGATTTTAAAGAAGAACTACAAAGAAGAATTTAAAAGAAGAATTTTAAAAGAAGAATTTTAAAAGAAG	1206  Qy 367 ATGARGANGATGATCTCAGAGGTGACGAGGGTCAGTGACGTTACCTACC	ACTGG 1266  Qy	AGCTC 1326 22 120 487 487 AGCTC 1320 Db 480	GAGTA 1386 CY 547 GAGTA 1380 Db 540
301 GACCTGATGTCTTTAAAGAGATGAGAGAAGCTTGGTGTCCCCAAGACCTGGAG 367 ATGAAGAAGATGATCTCAGAGGTGACAGGGGGTCAGTGACACTGATGACCAGAGAC 367 ATGAAGAAGATGATCTCAGAGGTGACAGGGGGTCAGTGACAGTGACATATCCTACCGAGAC 361 ATGAAGAAGATGATCTCAGAGGTGACAGGGGGTCAGTGACAGTGACATATCCTACCGAGAC	427 TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGT  421 TTTGTGAACATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGT  487 GGAAAAGCCAACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAG	547 AGCCTGCCCTGAGGACCCCGCCTGCCCAGCCTTCCCACCCCATACCTCCCTC	667 GGGTTTGTTTGTTGTTTTGTAATGTCTTTGTAAAGGACAAATTATCTGCCTTAAAGGGG 661 GGGTTTGTTTGTTTTCATCATGTCTTTTGTAAAGGACACAAATTATCTGCCTTAAAGGGG 727 CTCTGGGTATTGTTTTCATCATGTCTTTTGTAAAGCACAAATTATCTGCCTTTAAAGGGG 727 CTCTGGGTAATCCTGAGCCTTGGGTCCCTCCTTCTTCCCCCG	721 CICIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	847 GAGGCTTCCAGCTGTGTTCCCCTCACTTGGAGGAACCAGCACTCCCATCTTT 	907 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCCAGGCC 901 AGTCTCCAAGCCAAGTTCAGGCTCACTGACCTGGCTCTGACGAGGACCCAGGCC 907 GAGAAGACTAGAGAAGACTGACCTGAGCTCTTGACGAGGACCCAGGCC	961 GAGAAGACCTTGGAGTAGGGCTGCAGGGCCTCTTTCGGGTTTTCCTTGGA	1021 CCTGGTTCCAGTGTCTCTCTCTCTCTCTCTCGGCCCCCGGGGCCCCCGGGCCCCCGGGGCCCCCGGGGCCCC	1147 AGGAGCTTGGCATTGGGAGCCCTTCAAGAAGGTACCAGAAGGAACCCTCCAGTCCTGCTC 	1207 TCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAGCGTGCAGCCCTACTGTCCCTT	1267 GGCAGCAGAGGCTTCGGAGGCAGAGTGAGGCCTGGGGTTTGGGGGGAAAGGTC 	1327 AGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGACCAGGATGGGAAATGAG 

TITLE Compositions and methods relating to breast specific genes and JOURNAL Patent: WO 0240672-A 29 23-MAY-2002; PEATURES Location/Qualifiers 1. 3470   /organism="Homo sapiens" / /mol_type="unassigned DNA" / /db_xref="taxon:9606"	Query Match 95.8%; Score 1423.2; DB 6; Length 3470; Best Local Similarity 99.7%; Pred: No. 0; Matches 1436; Conservative 0; Mismatches 3; Indels 1; Gaps 1	Oy 32 CAGGGCCTGTGCTCCTCGTCCTCGCCGCGTCCGCGAAGCCTGGAGCCGGGGA 91	QY         92 GCCCGGGGTCGGGGCGAGCTCAGCAACAGGTTCCAAGGAAGG	QY         152 GCTTGCTCAAAGCCCGGCAGGAGGAGGGCTGGCCGAGATCAACCGGGAGTTTCTGTGTG         211           Db         122 GCTTGCTCAAAGCCCGGCAGGAGGGCTGGCCGAGATCAACCGGGAGTTTCTGTGTG         181	QY         212 ACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAGGTCACAGCTTCAAAGAGAAGT         271           Db         182 ACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAAGCTCACAGCCTTCAAAGAGAAAGT         241	Oy 272 ACAIGGAGTITGACCIGAACAAIGAAGGGAGATITGACCIGAIGICTITAAAGAGGAIGA 331	Oy 332 TGGAGAAGCTTGGTGTCCCCAAGACCTGGAGATGAAGAAGATGATCTCAGAGGTGA 391	Oy 392 CAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAACATGGTGGGGGAAAC 451	QY         452         GGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCAACGAGAGCACCCCA         511           Db         422         GGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCAACGAGAGCACCCCA         481	QY         512 AGCCAGTTGGCCCCTCCAGAGAGACATTGCTAGCCTGCCCTGAGGACCCCGCCTGG         571	Oy 572 ACTCCCCAGCCTTCCCACCCCATACCTCCCCGATCTTGCTGCCTTCTTGACACACT 631	Oy 632 GTGATCTCTCTCTCTTTTGTTTGTCTTGAGGGTTTGTTTG		Oy 812 AAACCAAAAACTAGAGGGGCAAGGGCCAGGGAGGGGTTCCAGCCTGTGTTCCCCTC 871  Db 782 AAACCAAAAACTAGAGGGGCCAGGGCCAGGGCAAGGGTTCCAGCCTGTGTTCCCCTC 841  Oy 872 ACTTGGAGGAACCACGCCCACGCCAGGGCTCCAAGCCTAGTTCCCCTC 841  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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lers sapiens" 9606" ,rebellum" rector: pME188FL3"  re 1399.4; DB 9; Length 1475;	Matches 1446; Conservative 0; Mismatches 6; Indels 25; Gaps 2; Caps	DD   121 CAGGTTCCAAGGCCGCCTCTTTGTCTCCCAGGAAGGCGTTCGCTTCCAAGG 180	0
B42 ACTTGGAGGAACCAGCACTCTCATCAGAAGTCTCCAAGCTAGGCTCA 901     QY	Qy         1112 CTTCTCATCCTCAGTGATGTGAAGGTGGGAAGGAAGGAAG	Qy         1292 AGTGAGGCCTGGGG-TTTGGGGGGAAAGGTCAGCTCATGTTCCACCTTTTAGGGAG 1350           Db         1262 AGTGAGGCCTGGGGTTTTGGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAG 1350           Db         1351 GATACTGAGGGACCAGGATGAGAAAGGTCAGGGTAAAATGCTCACGGCAAAGTCAGCAG 1321           Oy         1352 GATACTGAGGGACCAGGATGGGAAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAG 1381           Oy         1411 CACTGGTAAGCCAAGATGAGAAATACAAGGTTGTTGTCTGACCCCAATCTGCTTGAAA 1470           Db         1382 CACTGGTAAGCCAAGAATACAAGGTTGTTGTCTGACCCCAATCTGCTTGAAA 1470	AKO57789  AKO5778  AKO

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KARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEPDLNNEGEIDLMSLKRMM
EKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMPEGKANESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 25 Row: a Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13899240.
Location/Qualifiers
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                                                                                                                                                                                                               Mammalian
                                                                                                                                                                                                       Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
  Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14714398.
Contact: MGC help desk
Email: cgapbs-readil.nih.gov
Tissue Procurement: ATCC
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99.6%; Pred. No. 0;
iive 0; Mismatches
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/clone="IMAGE:3842109"
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                                                                                                                                                         Strausberg, R.
Direct Submission
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TITLE
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I (bases 1 to 1446)
Strauberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Alschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Villalon, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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                                                                                                                                                                                                                                                                                                                                                                CCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCCACACTCCTCTTCTCATCCTC 1123
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841 AGAGGGGCAGGCCAGGGCAGGCATCCCAGCCTGTGTTCCCCCTCACTTGGAGGAAC 900
                                                                              TGACGAGGACCCCAGGCCACTCTGAGAAGACCTTTGGAGTAGGGACAAGGCTGCAGGGCCT
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KEYWORDS
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	P2 CQ851292 ITON Sequence ION CQ851292 N CQ851292 NS CQ851292 NS Homo sapi MISM Homo sapi NS Hom	/mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN Query Match Best Local Similarity 94.9%; Pred. No. 0; Matches 1463; Conservative 0; Mismatches	Oy 7 ACACGCAGCTAGCCGGAGCCCGGACCAGGGCCTGTGCCTCCTCGTCGCCGCGCGCG	67	127	Qy 187 GAGATCAACCGDD 181 GAGATCAACCGGTACTGTGCCAGGAGGAGGAGCTACAGAGGATTTCATGTTCCCAG	Qy 198GGAGTITCTGTGTGACCAGAAGTACAGTGATT	Qy 229 GAAGAGCTTCCAGAAAAGCTCACAGCCTTCAAGAGAAGTACATGGAGTTTGACCTG	QY 289 AACAATGAAGGCGAGATTGACCTGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCTT 	Ay cccaagacccactggagargargaagargargargaggagagaggagtcagagagacccaccagagagagagag	Qy 409 ACTATATCCTACCGAGACTTTGTGAACATGGTGGGGGAAACGGTCGGCTGTCCTCAAG
Dy         206         TGTGTGACCAGAAGTACAGTGATGAAGAACCTTCCAGAAAAGCTCACAGCCTTCAAAG         265           Db         181         TGTGTGACCAGAAGTACAGTGAAGAACCTTCCAGAAAAGCTCCACAGCCTTCAAAG         240           181         TGTGTGACCAGAAGTACAGAAAAAAAAAGAATAGACCTGAATGTCTTTTAAAGA         240           Qy         266         AGAAGTACATGACGTTCGACCAAAAAAAAAAAAAAAAAA	361 AGGIGACAGGAGGGGTCAGTATACCTACCAGGACTTTGTGAACATGATGCTGG 361 AGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAACATGATGCTGG 446 GGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCAACGAGAGA 421 GGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATTGCTAGCTGCTGCAACGAGAGCA 506 GCCCCAAGCTTGGCCCCCTCCAGAGAGACATTGCTAGCTGCTGCCTGAGGAGCC 56 GCCCCAAGCCAGTTGGCCCCCTCCCAGAGAGACATTGCTAGCTGCTGCCTGAGGACCC 56 GCCCCAAGCCAGTTGGCCCCCCCCCCCCAACATTGCTAGCTTGCTAGCTGCTGAGAGACCC 56 GCCCCAAGCCAGCTTGCCCCCCCCCCCCCAACACTTGCTAGCTTGCTT	Qy         686         TCAALGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGCTCTGGGTCGGGGAATCCT         745           Db         661         TCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGAATCCT         720           Qy         746         GAGCCTTGGGTCCCTCTCTTCTTCTCCCTCTTCCCCGCTCCTGTGCAGAAGGGCT         805           Qy         16         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11         11	806 GATATCANACCANANATAGAGGGGGGGGGGGGGGCCAGGGGGGGGGG	OY 866 CCCCTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAGTCTCCAAGCTAGTTCA 925	Oy 926 GGCTCACTGACCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGG 985	Qy         986         GACAAGGCTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCTG         1045           D         1611111111111111111111111111111111111	Oy 1046 GIGICACCCAGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCACTCATTCC 1105	QY         1106         ACACCTCTTCTCATCTCAGTGATGTGAAGGTGGGAAGGAA	Qy         1166         CCCTTCAAGAAGGTACCAGAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAG         1225           Db         1141         CCCTTCAAGAAGGTACCAGAAGGAACCTCCAGTCCTGCTCTTGGCCACACTGTGCAG         1200	Oy 1226 GCAGCTGAGAGGCAGCGTGCACCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGA 1285	1286 G

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Submitted (15-701-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library of construction: Hellx Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.
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                PRI 19-FEB-2004
moderately
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                AK128526 3451 bp mRNA linear Homo sapiens cDNA FLJ46684 fis, clone TRACH3011282, similar to Allograft inflammatory factor-1.
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/note="cloning vector: pME18SFL3"
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AK128526.1 GI:34535937
oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Isogai, T. and Yamamoto, J.
Direct Submission
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Db 1261 AACCCTCAGTCCTGC Qy 1249 CCTACTGTCCCTTACT Db 1321 CCTACTGTCCCTTACT Qy 1309 GGGGGAAAGGTCAGG Qy 1309 GGGGGAAAGGTCAGG Qy 1369 ATGGGAGAATGAGGAC Qy 1369 ATGGGAGAATGAGGAC Qy 1369 ATGGGAGAATGAGGGAG Db 1441 ATGGGAGAATGAGGGTC Db 1429 GAGAAATACAAGGTTC Db 1501 GAGAAATACAAGGTTC Db 1501 GAGAAATACAAGGTTC	Search completed: March 29, 20 Job time: 6885 secs			
187 GAGATCAACCG		69 CCCCATACCTCCCCCGATCTTGCTGCCCTTCTTGACACTGTGATCTCTCTC	GGGCAGGGCAGGGAGGCTTCCAGCCTGTTCCCCTCACTTGGAGGAACCAGCAGCAGGCAG	1069 CGGGGCCCCGCTGCCCCAGCTGATCCCACTCTTCTCTCTC
8 4 8 4 8 4 8 4	8 6 8 6 8 6	6 6 6 6 6 6 6	8 6 8 6 8 6 8	6 8 6 8 6

Db 1261 AACCTCCAGTCCTGGCCACCTCTGCAGGCAGCTGAGAGGCAGCTGCAGC 1320

Oy 1249 CCTACTGTCCCTTACTGGCCACAGGGCTTCGGAGGCAGCTGCGGTTT 1308

Db 1321 CCTACTGTCCCTTACTGGGCAGCAGGGCTTCGGAGGCAGAAGTGAGGCCTGGGGTTT 1380

Oy 1309 GGGGGGAAAGGTCAGCTCATCTCACCTTTTAGGGAGGATACTGAGGGAACTTT 1380

Db 1381 GGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGCATACTGAGGGACCAGG 1440

Oy 1369 ATGGAGAAATGATGAGGTCAGTGCTGTTCCACCTTTTAGGGAGCATCTGAGGGGACCAGG 1440

Oy 1369 ATGGAGAAATGAGGGTCACTGGTACCAGCAGAGTGAGCAGGACCAGG 1420

Db 141 ATGGAGAAATACAAATGCTGACCCCAATGTGCTTGAAA 1470

Db 1501 GAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGTTGAAA 1542

Search completed: March 29, 2005, 03:23:36